

**RNA INTERFERENCE MEDIATED TREATMENT OF POLYGLUTAMINE
(POLYQ) REPEAT EXPANSION DISEASES USING SHORT INTERFERING
NUCLEIC ACID (siNA)**

This application is a continuation-in-part of U.S. Patent Application No. 10/783128, filed February 20, 2004, which is a continuation-in-part of U.S. Patent Application No. 10/757,803, filed January 14, 2004, which is a continuation-in-part of U.S. Patent Application No. 10/720,448, filed November 24, 2003, which is a continuation-in-part of U.S. Patent Application No. 10/693,059, filed October 23, 2003, which is a continuation-in-part of U.S. Patent Application No. 10/444,853, filed May 23, 2003 and a continuation-in-part of 10/652,791, filed August 29, 2003, which is a continuation of 10/422,704, filed April 24, 2003, which is a continuation of U.S. Patent Application No. 10/417,012, filed April 16, 2003. This application is also a continuation-in-part of International Patent Application No. PCT/US03/05346, filed February 20, 2003, and a continuation-in-part of International Patent Application No. PCT/US03/05028, filed February 20, 2003, both of which claim the benefit of U.S. Provisional Application No. 60/358,580 filed February 20, 2002, U.S. Provisional Application No. 60/363,124 filed March 11, 2002, U.S. Provisional Application No. 60/386,782 filed June 6, 2002, U.S. Provisional Application No. 60/406,784 filed August 29, 2002, U.S. Provisional Application No. 60/408,378 filed September 5, 2002, U.S. Provisional Application No. 60/409,293 filed September 9, 2002, and U.S. Provisional Application No. 60/440,129 filed January 15, 2003. This application is also a continuation-in-part of US Patent Application No. 10/427,160, filed April 30, 2003 and International Patent Application No. PCT/US02/15876 filed May 17, 2002. The instant application claims the benefit of all the listed applications, which are hereby incorporated by reference herein in their entireties, including the drawings.

Field Of The Invention

The present invention concerns compounds, compositions, and methods for the study, diagnosis, and treatment of diseases and conditions associated with polyglutamine repeat (polyQ) allelic variants that respond to the modulation of gene expression and/or activity. The present invention also concerns compounds, compositions, and methods

relating to diseases and conditions associated with polyglutamine repeat (polyQ) allelic variants that respond to the modulation of expression and/or activity of genes involved in polyQ repeat gene expression pathways or other cellular processes that mediate the maintenance or development of polyQ repeat diseases and conditions. Specifically, the invention relates to small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules capable of mediating RNA interference (RNAi) against the expression disease related genes or alleles having polyQ repeat sequences.

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Background Of The Invention

The following is a discussion of relevant art pertaining to RNAi. The discussion is provided only for understanding of the invention that follows. The summary is not an admission that any of the work described below is prior art to the claimed invention.

RNA interference refers to the process of sequence-specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Zamore *et al.*, 2000, *Cell*, 101, 25-33; Fire *et al.*, 1998, *Nature*, 391, 806; Hamilton *et al.*, 1999, *Science*, 286, 950-951). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes and is commonly shared by diverse flora and phyla (Fire *et al.*, 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or from the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response through a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2',5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Hamilton *et al.*, *supra*; Zamore *et al.*, 2000, *Cell*, 101, 25-33; Bernstein *et al.*, 2001, *Nature*, 409, 363). Short interfering RNAs derived from dicer activity are typically about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes (Hamilton *et al.*, *supra*; Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.*, 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex, commonly referred to as an RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence complementary to the antisense strand of the siRNA duplex. Cleavage of the target RNA takes place in the middle of the region complementary to the antisense strand of the siRNA duplex (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188).

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Bahramian and Zarbl, 1999, *Molecular and Cellular Biology*, 19, 274-283 and Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mammalian systems. Hammond *et al.*, 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.*, 2001, *Nature*, 411, 494 and Tuschl *et al.*, International PCT Publication No. WO 01/75164, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877 and Tuschl *et al.*, International PCT Publication No. WO 01/75164) has revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21-nucleotide siRNA duplexes are most active when containing 3'-terminal dinucleotide overhangs. Furthermore, complete substitution of one or both siRNA strands with 2'-deoxy (2'-H) or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of the 3'-terminal siRNA overhang nucleotides with 2'-deoxy nucleotides (2'-H) was shown to be tolerated. Single mismatch sequences in the center of the siRNA duplex were also

shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end of the guide sequence (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.*, 2001, *Cell*, 107, 309).

Studies have shown that replacing the 3'-terminal nucleotide overhanging segments of a 21-mer siRNA duplex having two-nucleotide 3'-overhangs with deoxyribonucleotides does not have an adverse effect on RNAi activity. Replacing up to four nucleotides on each end of the siRNA with deoxyribonucleotides has been reported to be well tolerated, whereas complete substitution with deoxyribonucleotides results in no RNAi activity (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877 and Tuschl *et al.*, International PCT Publication No. WO 01/75164). In addition, Elbashir *et al.*, *supra*, also report that substitution of siRNA with 2'-O-methyl nucleotides completely abolishes RNAi activity. Li *et al.*, International PCT Publication No. WO 00/44914, and Beach *et al.*, International PCT Publication No. WO 01/68836 preliminarily suggest that siRNA may include modifications to either the phosphate-sugar backbone or the nucleoside to include at least one of a nitrogen or sulfur heteroatom, however, neither application postulates to what extent such modifications would be tolerated in siRNA molecules, nor provides any further guidance or examples of such modified siRNA. Kreutzer *et al.*, Canadian Patent Application No. 2,359,180, also describe certain chemical modifications for use in dsRNA constructs in order to counteract activation of double-stranded RNA-dependent protein kinase PKR, specifically 2'-amino or 2'-O-methyl nucleotides, and nucleotides containing a 2'-O or 4'-C methylene bridge. However, Kreutzer *et al.* similarly fails to provide examples or guidance as to what extent these modifications would be tolerated in dsRNA molecules.

Parrish *et al.*, 2000, *Molecular Cell*, 6, 1077-1087, tested certain chemical modifications targeting the *unc-22* gene in *C. elegans* using long (>25 nt) siRNA transcripts. The authors describe the introduction of thiophosphate residues into these siRNA transcripts by incorporating thiophosphate nucleotide analogs with T7 and T3 RNA polymerase and observed that RNAs with two phosphorothioate modified bases

also had substantial decreases in effectiveness as RNAi. Further, Parrish *et al.* reported that phosphorothioate modification of more than two residues greatly destabilized the RNAs *in vitro* such that interference activities could not be assayed. *Id.* at 1081. The authors also tested certain modifications at the 2'-position of the nucleotide sugar in the long siRNA transcripts and found that substituting deoxynucleotides for ribonucleotides produced a substantial decrease in interference activity, especially in the case of Uridine to Thymidine and/or Cytidine to deoxy-Cytidine substitutions. *Id.* In addition, the authors tested certain base modifications, including substituting, in sense and antisense strands of the siRNA, 4-thiouracil, 5-bromouracil, 5-iodouracil, and 3-(aminoallyl)uracil for uracil, and inosine for guanosine. Whereas 4-thiouracil and 5-bromouracil substitution appeared to be tolerated, Parrish reported that inosine produced a substantial decrease in interference activity when incorporated in either strand. Parrish also reported that incorporation of 5-iodouracil and 3-(aminoallyl)uracil in the antisense strand resulted in a substantial decrease in RNAi activity as well.

The use of longer dsRNA has been described. For example, Beach *et al.*, International PCT Publication No. WO 01/68836, describes specific methods for attenuating gene expression using endogenously-derived dsRNA. Tuschl *et al.*, International PCT Publication No. WO 01/75164, describe a *Drosophila in vitro* RNAi system and the use of specific siRNA molecules for certain functional genomic and certain therapeutic applications; although Tuschl, 2001, *Chem. Biochem.*, 2, 239-245, doubts that RNAi can be used to cure genetic diseases or viral infection due to the danger of activating interferon response. Li *et al.*, International PCT Publication No. WO 00/44914, describe the use of specific long (141 bp-488 bp) enzymatically synthesized or vector expressed dsRNAs for attenuating the expression of certain target genes. Zernicka-Goetz *et al.*, International PCT Publication No. WO 01/36646, describe certain methods for inhibiting the expression of particular genes in mammalian cells using certain long (550 bp-714 bp), enzymatically synthesized or vector expressed dsRNA molecules. Fire *et al.*, International PCT Publication No. WO 99/32619, describe particular methods for introducing certain long dsRNA molecules into cells for use in inhibiting gene expression in nematodes. Plaetinck *et al.*, International PCT Publication No. WO 00/01846, describe certain methods for identifying specific genes responsible for conferring a particular phenotype in a cell using specific long dsRNA molecules.

- Mello *et al.*, International PCT Publication No. WO 01/29058, describe the identification of specific genes involved in dsRNA-mediated RNAi. Deschamps Depaillette *et al.*, International PCT Publication No. WO 99/07409, describe specific compositions consisting of particular dsRNA molecules combined with certain anti-viral agents.
- 5 Waterhouse *et al.*, International PCT Publication No. 99/53050, describe certain methods for decreasing the phenotypic expression of a nucleic acid in plant cells using certain dsRNAs. Driscoll *et al.*, International PCT Publication No. WO 01/49844, describe specific DNA expression constructs for use in facilitating gene silencing in targeted organisms.
- 10 Others have reported on various RNAi and gene-silencing systems. For example, Parrish *et al.*, 2000, *Molecular Cell*, 6, 1077-1087, describe specific chemically-modified dsRNA constructs targeting the *unc-22* gene of *C. elegans*. Grossniklaus, International PCT Publication No. WO 01/38551, describes certain methods for regulating polycomb gene expression in plants using certain dsRNAs. Churikov *et al.*, International PCT
- 15 Publication No. WO 01/42443, describe certain methods for modifying genetic characteristics of an organism using certain dsRNAs. Cogoni *et al.*, International PCT Publication No. WO 01/53475, describe certain methods for isolating a *Neurospora* silencing gene and uses thereof. Reed *et al.*, International PCT Publication No. WO 01/68836, describe certain methods for gene silencing in plants. Honer *et al.*,
- 20 International PCT Publication No. WO 01/70944, describe certain methods of drug screening using transgenic nematodes as Parkinson's Disease models using certain dsRNAs. Deak *et al.*, International PCT Publication No. WO 01/72774, describe certain *Drosophila*-derived gene products that may be related to RNAi in *Drosophila*. Arndt *et al.*, International PCT Publication No. WO 01/92513 describe certain methods for
- 25 mediating gene suppression by using factors that enhance RNAi. Tuschl *et al.*, International PCT Publication No. WO 02/44321, describe certain synthetic siRNA constructs. Pachuk *et al.*, International PCT Publication No. WO 00/63364, and Satishchandran *et al.*, International PCT Publication No. WO 01/04313, describe certain methods and compositions for inhibiting the function of certain polynucleotide
- 30 sequences using certain long (over 250 bp), vector expressed dsRNAs. Echeverri *et al.*, International PCT Publication No. WO 02/38805, describe certain *C. elegans* genes identified via RNAi. Kreutzer *et al.*, International PCT Publications Nos. WO

02/055692, WO 02/055693, and EP 1144623 B1 describes certain methods for inhibiting gene expression using dsRNA. Graham *et al.*, International PCT Publications Nos. WO 99/49029 and WO 01/70949, and AU 4037501 describe certain vector expressed siRNA molecules. Fire *et al.*, US 6,506,559, describe certain methods for inhibiting gene expression in vitro using certain long dsRNA (299 bp-1033 bp) constructs that mediate RNAi. Martinez *et al.*, 2002, *Cell*, 110, 563-574, describe certain single stranded siRNA constructs, including certain 5'-phosphorylated single stranded siRNAs that mediate RNA interference in Hela cells. Harborth *et al.*, 2003, *Antisense & Nucleic Acid Drug Development*, 13, 83-105, describe certain chemically and structurally modified siRNA molecules. Chiu and Rana, 2003, *RNA*, 9, 1034-1048, describe certain chemically and structurally modified siRNA molecules. Miller *et al.*, 2003, *PNAS*, 100, 7195-7200, describe certain transcribed siRNA molecules targeting certain allele specific RNA transcripts associated with trinucleotide repeat/polyQ neurodegenerative disorders such as Machado Joseph Disease, spinocerebellar ataxia, and frontotemporal dementia. Davidson *et al.*, WO 04/013280, describe certain siRNA molecules targeting certain allele specific RNA transcripts including certain polyQ repeat gene transcripts associated with certain neurodegenerative diseases.

SUMMARY OF THE INVENTION

This invention relates to compounds, compositions, and methods useful for modulating the expression of repeat expansion genes associated with the maintenance or development of neurodegenerative disease, for example polyglutamine repeat expansion genes and variants thereof, including single nucleotide polymorphism (SNP) variants associated with disease related trinucleotide repeat expansion genes, using short interfering nucleic acid (siNA) molecules. This invention also relates to compounds, compositions, and methods useful for modulating the expression and activity of repeat expansion genes, or other genes involved in pathways of repeat expansion genes expression and/or activity by RNA interference (RNAi) using small nucleic acid molecules. In particular, the instant invention features small nucleic acid molecules, such as short interfering nucleic acid (siNA), short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), and short hairpin RNA (shRNA) molecules and methods used to modulate the expression of repeat expansion genes. A

siNA of the invention can be unmodified or chemically-modified. A siNA of the instant invention can be chemically synthesized, expressed from a vector or enzymatically synthesized. The instant invention also features various chemically-modified synthetic short interfering nucleic acid (siNA) molecules capable of modulating repeat expansion gene expression or activity in cells by RNA interference (RNAi). The use of chemically-modified siNA improves various properties of native siNA molecules through increased resistance to nuclease degradation *in vivo* and/or through improved cellular uptake. Further, contrary to earlier published studies, siNA having multiple chemical modifications retains its RNAi activity. The siNA molecules of the instant invention provide useful reagents and methods for a variety of therapeutic, diagnostic, target validation, genomic discovery, genetic engineering, and pharmacogenomic applications.

In one embodiment, the invention features one or more siNA molecules and methods that independently or in combination modulate the expression of repeat expansion genes encoding proteins, such as proteins comprising polyglutamine repeat expansions, associated with the maintenance and/or development of neurodegenerative diseases, such as genes encoding sequences comprising those sequences referred to by GenBank Accession Nos. shown in **Table I**, referred to herein generally as repeat expansion (RE) genes. The description below of the various aspects and embodiments of the invention is provided with reference to exemplary Huntingtin gene referred to herein as HD. However, the various aspects and embodiments are also directed to other repeat expansion genes, such spinocerebellar ataxia genes including SCA1, SCA2, SCA3, SCA5, SCA7, SCA12, and SCA17, spinal and bulbar muscular atrophy genes such as androgen receptor (*AR*) locus Xq11-q12 genes, and dentatorubropallidoluysian atrophy genes such as DRPLA, as well as other mutant gene variants having trinucleotide repeat expansions and SNPs associated with such trinucleotide repeat expansions.. The various aspects and embodiments are also directed to other genes that are involved in RE mediated pathways of signal transduction or gene expression that are involved in the progression, development, and/or maintenance of disease (e.g., Huntington disease, spinocerebellar ataxia, spinal and bulbar muscular dystrophy, and dentatorubropallidoluysian atrophy), including enzymes involved in processing RE proteins. These additional genes can be analyzed for target sites using the methods described for HD genes herein. Thus, the modulation of other genes and the effects of

such modulation of the other genes can be performed, determined, and measured as described herein.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a repeat expansion (RE) gene, wherein said siNA molecule comprises about 19 to about 21 base pairs.

In one embodiment, the invention features a siNA molecule that down-regulates expression of a RE gene, for example, wherein the RE gene comprises RE encoding sequence. In one embodiment, the invention features a siNA molecule that down-regulates expression of a RE gene, for example, wherein the RE gene comprises RE non-coding sequence or regulatory elements involved in RE gene expression.

In one embodiment, the invention features a siNA molecule having RNAi activity against RE RNA, wherein the siNA molecule comprises a sequence complementary to any RNA having RE encoding sequence, such as those sequences having GenBank Accession Nos. shown in **Table I**. In another embodiment, the invention features a siNA molecule having RNAi activity against RE RNA, wherein the siNA molecule comprises a sequence complementary to an RNA having other RE encoding sequence, for example other mutant RE genes not shown in Table I but known in the art to be associated with the development or maintenance of repeat expansion diseases and conditions, such as Huntington disease, spinocerebellar ataxia, spinal and bulbar muscular dystrophy, and dentatorubropallidoluysian atrophy. Chemical modifications as shown in **Tables III and IV** or otherwise described herein can be applied to any siNA construct of the invention. In another embodiment, a siNA molecule of the invention includes nucleotide sequence that can interact with nucleotide sequence of a RE gene and thereby mediate silencing of RE gene expression, for example, wherein the siNA mediates regulation of RE gene expression by cellular processes that modulate the chromatin structure of the RE gene and prevent transcription of the RE gene.

In one embodiment, siNA molecules of the invention are used to down regulate or inhibit the expression of mutant RE proteins that are neurotoxic, such as mutant RE proteins resulting from polyglutamine repeat expansions and fragments or portions of such mutant RE proteins that are processed by cellular enzymes resulting in neurotoxic

proteins or peptides. Analysis of RE genes, or RE protein or RNA levels can be used to identify subjects with Huntington disease or at risk of developing Huntington disease. These subjects are amenable to treatment, for example, treatment with siNA molecules of the invention and any other composition useful in treating Huntington disease. As such, analysis of RE protein or RNA levels can be used to determine treatment type and the course of therapy in treating a subject. Monitoring of RE protein or RNA levels can be used to predict treatment outcome and to determine the efficacy of compounds and compositions that modulate the level and/or activity of certain RE proteins associated with disease.

10 In another embodiment, the invention features a siNA molecule comprising nucleotide sequence, for example, nucleotide sequence in the antisense region of the siNA molecule that is complementary to a nucleotide sequence or portion of sequence of a RE gene. In another embodiment, the invention features a siNA molecule comprising a region, for example, the antisense region of the siNA construct, complementary to a sequence comprising a RE gene sequence or a portion thereof.

In one embodiment, the antisense region of RE siNA constructs can comprise a sequence complementary to sequence having any of SEQ ID NOs. 1-1752 and 3505-3511. In one embodiment, the antisense region can also comprise sequence having any of SEQ ID NOs. 1753-3504, 3513, 3515, 3517, 3530-3535, 3542-3547, 3554-3559, 3570, 3572, 3574, or 3577. In another embodiment, the sense region of the RE constructs can comprise sequence having any of SEQ ID NOs. 1-1752, 3505-3511, 3512, 3514, 3516, 3524-3529, 3536-3541, 3548-3553, 3569, 3571, 3573, 3575, or 3576. The sense region can comprise a sequence of SEQ ID NO. 3560 and the antisense region can comprise a sequence of SEQ ID NO. 3561. The sense region can comprise a sequence of SEQ ID NO. 3562 and the antisense region can comprise a sequence of SEQ ID NO. 3563. The sense region can comprise a sequence of SEQ ID NO. 3564 and the antisense region can comprise a sequence of SEQ ID NO. 3565. The sense region can comprise a sequence of SEQ ID NO. 3566 and the antisense region can comprise a sequence of SEQ ID NO. 3563. The sense region can comprise a sequence of SEQ ID NO. 3567 and the antisense region can comprise a sequence of SEQ ID NO. 3563. The sense region can

comprise a sequence of SEQ ID NO. 3566 and the antisense region can comprise a sequence of SEQ ID NO. 3568.

In one embodiment, a siNA molecule of the invention comprises any of SEQ ID NOs. 1-3577. The sequences shown in SEQ ID NOs: 1-3577 are not limiting. A siNA molecule of the invention can comprise any contiguous RE sequence (e.g., about 19 to about 25, or about 19, 20, 21, 22, 23, 24 or 25 contiguous RE nucleotides).

In yet another embodiment, the invention features a siNA molecule comprising a sequence, for example, the antisense sequence of the siNA construct, complementary to a sequence or portion of sequence comprising sequence represented by GenBank Accession Nos. shown in **Table I**. Chemical modifications in **Tables III and IV** and described herein can be applied to any siNA construct of the invention.

In one embodiment of the invention a siNA molecule comprises an antisense strand having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29) nucleotides, wherein the antisense strand is complementary to a RNA sequence encoding a RE protein, and wherein said siNA further comprises a sense strand having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, and wherein said sense strand and said antisense strand are distinct nucleotide sequences with at least about 19 complementary nucleotides.

In another embodiment of the invention a siNA molecule of the invention comprises an antisense region having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or 29) nucleotides, wherein the antisense region is complementary to a RNA sequence encoding a RE protein, and wherein said siNA further comprises a sense region having about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or more) nucleotides, wherein said sense region and said antisense region comprise a linear molecule with at least about 19 complementary nucleotides.

In one embodiment of the invention a siNA molecule comprises an antisense strand comprising a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof encoding a RE protein. The siNA further comprises a sense strand,

wherein said sense strand comprises a nucleotide sequence of a RE gene or a portion thereof.

In another embodiment, a siNA molecule comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence
5 encoding a RE protein or a portion thereof. The siNA molecule further comprises a sense region, wherein said sense region comprises a nucleotide sequence of a RE gene or a portion thereof.

In one embodiment, a siNA molecule of the invention has RNAi activity that modulates expression of RNA encoded by a RE gene. Because RE genes can share some
10 degree of sequence homology with each other, siNA molecules can be designed to target a class of RE genes or alternately specific RE genes (e.g., SNP variants) by selecting sequences that are either shared amongst different RE targets or alternatively that are unique for a specific RE target. Therefore, in one embodiment, the siNA molecule can be designed to target conserved regions of RE RNA sequence having homology between
15 several RE gene variants so as to target a class of RE genes (e.g., RE variants having differing trinucleotide repeat expansions) with one siNA molecule. Accordingly, in one embodiment, the siNA molecule of the invention modulates the expression of one or both RE alleles in a subject. In another embodiment, the siNA molecule can be designed to target a sequence that is unique to a specific RE RNA sequence (e.g., a single RE
20 allele or RE SNP) due to the high degree of specificity that the siNA molecule requires to mediate RNAi activity

In one embodiment, nucleic acid molecules of the invention that act as mediators of the RNA interference gene silencing response are double-stranded nucleic acid molecules. In another embodiment, the siNA molecules of the invention consist of
25 duplexes containing about 19 base pairs between oligonucleotides comprising about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24 or 25) nucleotides. In yet another embodiment, siNA molecules of the invention comprise duplexes with overhanging ends of about about 1 to about 3 (e.g., about 1, 2, or 3) nucleotides, for example, about 21-nucleotide duplexes with about 19 base pairs and 3'-terminal mononucleotide,
30 dinucleotide, or trinucleotide overhangs.

In one embodiment, the invention features one or more chemically-modified siNA constructs having specificity for RE expressing nucleic acid molecules, such as RNA encoding a RE protein. Non-limiting examples of such chemical modifications include without limitation phosphorothioate internucleotide linkages, 2'-deoxyribonucleotides, 2'-O-methyl ribonucleotides, 2'-deoxy-2'-fluoro ribonucleotides, "universal base" nucleotides, "acyclic" nucleotides, 5-C-methyl nucleotides, and terminal glyceryl and/or inverted deoxy abasic residue incorporation. These chemical modifications, when used in various siNA constructs, are shown to preserve RNAi activity in cells while at the same time, dramatically increasing the serum stability of these compounds. Furthermore, contrary to the data published by Parrish *et al.*, *supra*, applicant demonstrates that multiple (greater than one) phosphorothioate substitutions are well-tolerated and confer substantial increases in serum stability for modified siNA constructs.

In one embodiment, a siNA molecule of the invention comprises modified nucleotides while maintaining the ability to mediate RNAi. The modified nucleotides can be used to improve *in vitro* or *in vivo* characteristics such as stability, activity, and/or bioavailability. For example, a siNA molecule of the invention can comprise modified nucleotides as a percentage of the total number of nucleotides present in the siNA molecule. As such, a siNA molecule of the invention can generally comprise about 5% to about 100% modified nucleotides (e.g., 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% modified nucleotides). The actual percentage of modified nucleotides present in a given siNA molecule will depend on the total number of nucleotides present in the siNA. If the siNA molecule is single stranded, the percent modification can be based upon the total number of nucleotides present in the single stranded siNA molecules. Likewise, if the siNA molecule is double stranded, the percent modification can be based upon the total number of nucleotides present in the sense strand, antisense strand, or both the sense and antisense strands.

One aspect of the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a RE gene. In one embodiment, a double stranded siNA molecule comprises one or more chemical modifications and

each strand of the double-stranded siNA is about 21 nucleotides long. In one embodiment, the double-stranded siNA molecule does not contain any ribonucleotides. In another embodiment, the double-stranded siNA molecule comprises one or more ribonucleotides. In one embodiment, each strand of the double-stranded siNA molecule comprises about 19 to about 23 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29) nucleotides, wherein each strand comprises about 19 nucleotides that are complementary to the nucleotides of the other strand. In one embodiment, one of the strands of the double-stranded siNA molecule comprises a nucleotide sequence that is complementary to a nucleotide sequence or a portion thereof of the RE gene, and the second strand of the double-stranded siNA molecule comprises a nucleotide sequence substantially similar to the nucleotide sequence of the RE gene or a portion thereof.

In another embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a RE gene comprising an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of the RE gene or a portion thereof, and a sense region, wherein the sense region comprises a nucleotide sequence substantially similar to the nucleotide sequence of the RE gene or a portion thereof. In one embodiment, the antisense region and the sense region each comprise about 19 to about 23 (e.g. about 19, 20, 21, 22, or 23) nucleotides, wherein the antisense region comprises about 19 nucleotides that are complementary to nucleotides of the sense region.

In another embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a RE gene comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the RE gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region.

In one embodiment, a siNA molecule of the invention comprises blunt ends, i.e., ends that do not include any overhanging nucleotides. For example, a siNA molecule of the invention comprising modifications described herein (e.g., comprising nucleotides having Formulae I-VII or siNA constructs comprising Stab00-Stab22 or any combination

thereof) and/or any length described herein can comprise blunt ends or ends with no overhanging nucleotides.

In one embodiment, any siNA molecule of the invention can comprise one or more blunt ends, i.e. where a blunt end does not have any overhanging nucleotides. In a non-limiting example, a blunt ended siNA molecule has a number of base pairs equal to the number of nucleotides present in each strand of the siNA molecule. In another example, a siNA molecule comprises one blunt end, for example wherein the 5'-end of the antisense strand and the 3'-end of the sense strand do not have any overhanging nucleotides. In another example, a siNA molecule comprises one blunt end, for example wherein the 3'-end of the antisense strand and the 5'-end of the sense strand do not have any overhanging nucleotides. In another example, a siNA molecule comprises two blunt ends, for example wherein the 3'-end of the antisense strand and the 5'-end of the sense strand as well as the 5'-end of the antisense strand and 3'-end of the sense strand do not have any overhanging nucleotides. A blunt ended siNA molecule can comprise, for example, from about 18 to about 30 nucleotides (e.g., about 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides). Other nucleotides present in a blunt ended siNA molecule can comprise mismatches, bulges, loops, or wobble base pairs, for example, to modulate the activity of the siNA molecule to mediate RNA interference.

By "blunt ends" is meant symmetric termini or termini of a double stranded siNA molecule having no overhanging nucleotides. The two strands of a double stranded siNA molecule align with each other without over-hanging nucleotides at the termini. For example, a blunt ended siNA construct comprises terminal nucleotides that are complementary between the sense and antisense regions of the siNA molecule.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a RE gene, wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule. The sense region can be connected to the antisense region via a linker molecule, such as a polynucleotide linker or a non-nucleotide linker.

In one embodiment, the invention features double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a repeat expansion (RE) gene, wherein the siNA molecule comprises about 19 to about 21 base pairs, and wherein each strand of the siNA molecule comprises one or more chemical modifications. In
5 another embodiment, one of the strands of the double-stranded siNA molecule comprises a nucleotide sequence that is complementary to a nucleotide sequence of a RE gene or a portion thereof, and the second strand of the double-stranded siNA molecule comprises a nucleotide sequence substantially similar to the nucleotide sequence or a portion thereof of the RE gene. In another embodiment, one of the strands of the double-stranded siNA
10 molecule comprises a nucleotide sequence that is complementary to a nucleotide sequence of a RE gene or a portion thereof, and the second strand of the double-stranded siNA molecule comprises a nucleotide sequence substantially similar to the nucleotide sequence or a portion thereof of the RE gene. In another embodiment, each strand of the siNA molecule comprises about 19 to about 23 nucleotides, and each strand comprises at
15 least about 19 nucleotides that are complementary to the nucleotides of the other strand. The RE gene can comprise, for example, huntingtin, SCA1, SCA2, SCA3, SCA6, SCA7, SCA12, SCA17, SBMA, or DRPLA (see for example Table I).

In one embodiment, a siNA molecule of the invention comprises no ribonucleotides. In another embodiment, a siNA molecule of the invention comprises
20 ribonucleotides.

In one embodiment, a siNA molecule of the invention comprises an antisense region comprising a nucleotide sequence that is complementary to a nucleotide sequence of a RE gene or a portion thereof, and the siNA further comprises a sense region comprising a nucleotide sequence substantially similar to the nucleotide sequence of the
25 RE gene or a portion thereof. In another embodiment, the antisense region and the sense region each comprise about 19 to about 23 nucleotides and the antisense region comprises at least about 19 nucleotides that are complementary to nucleotides of the sense region. The RE gene can comprise, for example, huntingtin, SCA1, SCA2, SCA3, SCA6, SCA7, SCA12, SCA17, SBMA, or DRPLA (see for example Table I).

30 In one embodiment, a siNA molecule of the invention comprises a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence

that is complementary to a nucleotide sequence of RNA encoded by a RE gene, or a portion thereof, and the sense region comprises a nucleotide sequence that is complementary to the antisense region. In another embodiment, the siNA molecule is assembled from two separate oligonucleotide fragments, wherein one fragment
5 comprises the sense region and the second fragment comprises the antisense region of the siNA molecule. In another embodiment, the sense region is connected to the antisense region via a linker molecule. In another embodiment, the sense region is connected to the antisense region via a linker molecule, such as a nucleotide or non-nucleotide linker. The RE gene can comprise, for example, huntingtin, SCA1, SCA2,
10 SCA3, SCA6, SCA7, SCA12, SCA17, SBMA, or DRPLA (see for example Table I).

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a RE gene comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by
15 the RE gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein the siNA molecule has one or more modified pyrimidine and/or purine nucleotides. In one embodiment, the pyrimidine nucleotides in the sense region are 2'-O-methyl pyrimidine nucleotides or 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense
20 region are 2'-deoxy purine nucleotides. In another embodiment, the pyrimidine nucleotides in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides. In another embodiment, the pyrimidine nucleotides in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are
25 2'-deoxy purine nucleotides. In one embodiment, the pyrimidine nucleotides in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the antisense region are 2'-O-methyl or 2'-deoxy purine nucleotides. In another embodiment of any of the above-described siNA molecules, any nucleotides present in a non-complementary region of the sense strand (e.g. overhang region) are 2'-
30 deoxy nucleotides.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a RE gene, wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule, and wherein the fragment comprising the sense region includes a terminal cap moiety at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the fragment. In another embodiment, the terminal cap moiety is an inverted deoxy abasic moiety or glyceryl moiety. In another embodiment, each of the two fragments of the siNA molecule comprise about 21 nucleotides.

10 In one embodiment, the invention features a siNA molecule comprising at least one modified nucleotide, wherein the modified nucleotide is a 2'-deoxy-2'-fluoro nucleotide. The siNA can be, for example, of length between about 12 and about 36 nucleotides. In another embodiment, all pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In another embodiment, the modified nucleotides in the siNA include at least one 2'-deoxy-2'-fluoro cytidine or 2'-deoxy-2'-fluoro uridine nucleotide. In another embodiment, the modified nucleotides in the siNA include at least one 2'-fluoro cytidine and at least one 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all uridine nucleotides present in the siNA are 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all cytidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro cytidine nucleotides. In another embodiment, all adenosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro adenosine nucleotides. In another embodiment, all guanosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro guanosine nucleotides. The siNA can further comprise at least one modified internucleotidic linkage, such as phosphorothioate linkage. In another embodiment, the 2'-deoxy-2'-fluoronucleotides are present at specifically selected locations in the siNA that are sensitive to cleavage by ribonucleases, such as locations having pyrimidine nucleotides.

20 In one embodiment, the invention features a method of increasing the stability of a siNA molecule against cleavage by ribonucleases comprising introducing at least one modified nucleotide into the siNA molecule, wherein the modified nucleotide is a 2'-deoxy-2'-fluoro nucleotide. In another embodiment, all pyrimidine nucleotides present

in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides. In another embodiment, the modified nucleotides in the siNA include at least one 2'-deoxy-2'-fluoro cytidine or 2'-deoxy-2'-fluoro uridine nucleotide. In another embodiment, the modified nucleotides in the siNA include at least one 2'-fluoro cytidine and at least one 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all uridine nucleotides present in the siNA are 2'-deoxy-2'-fluoro uridine nucleotides. In another embodiment, all cytidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro cytidine nucleotides. In another embodiment, all adenosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro adenosine nucleotides. In another embodiment, all guanosine nucleotides present in the siNA are 2'-deoxy-2'-fluoro guanosine nucleotides. The siNA can further comprise at least one modified internucleotidic linkage, such as phosphorothioate linkage. In another embodiment, the 2'-deoxy-2'-fluoronucleotides are present at specifically selected locations in the siNA that are sensitive to cleavage by ribonucleases, such as locations having pyrimidine nucleotides.

15 In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a RE gene comprising a sense region and an antisense region, wherein the antisense region comprises a nucleotide sequence that is complementary to a nucleotide sequence of RNA encoded by the RE gene or a portion thereof and the sense region comprises a nucleotide sequence that is complementary to the antisense region, and wherein the purine nucleotides present in the antisense region comprise 2'-deoxy- purine nucleotides. In an alternative embodiment, the purine nucleotides present in the antisense region comprise 2'-O-methyl purine nucleotides. In either of the above embodiments, the antisense region can comprise a phosphorothioate internucleotide linkage at the 3' end of the antisense region.

20

25 Alternatively, in either of the above embodiments, the antisense region can comprise a glyceryl modification at the 3' end of the antisense region. In another embodiment of any of the above-described siNA molecules, any nucleotides present in a non-complementary region of the antisense strand (e.g. overhang region) are 2'-deoxy nucleotides.

30 In one embodiment, the antisense region of a siNA molecule of the invention comprises sequence complementary to a portion of a RE transcript having sequence

comprising the repeat expansion or a portion thereof and sequence unique to the particular RE disease related allele (e.g., huntingtin), such as sequence adjacent to the repeat expansion (e.g., adjacent to the 5' or 3' portion of the repeat expansion) or sequence comprising a SNP associated with the disease specific allele. As such, the antisense region of a siNA molecule of the invention can comprise sequence complementary to a repeat expansion region and adjacent sequences that are unique to a particular allele to provide specificity in mediating selective RNAi against the disease related allele.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that down-regulates expression of a RE gene, wherein the siNA molecule is assembled from two separate oligonucleotide fragments wherein one fragment comprises the sense region and the second fragment comprises the antisense region of the siNA molecule. In another embodiment about 19 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule and wherein at least two 3' terminal nucleotides of each fragment of the siNA molecule are not base-paired to the nucleotides of the other fragment of the siNA molecule. In one embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-deoxy-pyrimidine nucleotide, such as a 2'-deoxy-thymidine. In another embodiment, all 21 nucleotides of each fragment of the siNA molecule are base-paired to the complementary nucleotides of the other fragment of the siNA molecule. In another embodiment, about 19 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the RNA encoded by the RE gene. In another embodiment, about 21 nucleotides of the antisense region are base-paired to the nucleotide sequence or a portion thereof of the RNA encoded by the RE gene. In any of the above embodiments, the 5'-end of the fragment comprising said antisense region can optionally includes a phosphate group.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits the expression of a RE RNA sequence (e.g., wherein said target RNA sequence is encoded by a RE gene involved in the RE pathway), wherein the siNA molecule does not contain any ribonucleotides and wherein each strand of the double-stranded siNA molecule is about 21 nucleotides long.

Examples of non-ribonucleotide containing siNA constructs are combinations of stabilization chemistries shown in Table IV in any combination of Sense/Antisense chemistries, such as Stab 7/8, Stab 7/11, Stab 8/8, Stab 18/8, Stab 18/11, Stab 12/13, Stab 7/13, Stab 18/13, Stab 7/19, Stab 8/19, Stab 18/19, Stab 7/20, Stab 8/20, or Stab 18/20.

In one embodiment, the invention features a chemically synthesized double stranded RNA molecule that directs cleavage of a RE RNA via RNA interference, wherein each strand of said RNA molecule is about 21 to about 23 nucleotides in length; one strand of the RNA molecule comprises nucleotide sequence having sufficient complementarity to the RE RNA for the RNA molecule to direct cleavage of the RE RNA via RNA interference; and wherein at least one strand of the RNA molecule comprises one or more chemically modified nucleotides described herein, such as deoxynucleotides, 2'-O-methyl nucleotides, 2'-deoxy-2'-fluoro nucleotides, 2'-O-methoxyethyl nucleotides etc.

In one embodiment, the invention features a medicament comprising a siNA molecule of the invention.

In one embodiment, the invention features an active ingredient comprising a siNA molecule of the invention.

In one embodiment, the invention features the use of a double-stranded short interfering nucleic acid (siNA) molecule to down-regulate expression of a RE gene, wherein the siNA molecule comprises one or more chemical modifications and each strand of the double-stranded siNA is about 18 to about 28 or more (e.g., 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28 or more) nucleotides long.

In one embodiment, the invention features the use of a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a RE gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of RE RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and

wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a RE gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of RE RNA or a portion thereof, wherein the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a RE gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of RE RNA that encodes a protein or portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a RE gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of RE RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification. In one embodiment, each strand of the siNA molecule comprises about 18 to about 29 or more (e.g., about 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or more) nucleotides, wherein each strand comprises at least about 18 nucleotides that are complementary to the nucleotides of the other strand. In another embodiment, the siNA molecule is assembled from two oligonucleotide fragments, wherein one fragment comprises the nucleotide sequence of the antisense strand of the siNA molecule and a

second fragment comprises nucleotide sequence of the sense region of the siNA molecule. In yet another embodiment, the sense strand is connected to the antisense strand via a linker molecule, such as a polynucleotide linker or a non-nucleotide linker. In a further embodiment, the pyrimidine nucleotides present in the sense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-deoxy purine nucleotides. In another embodiment, the pyrimidine nucleotides present in the sense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and the purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides. In still another embodiment, the pyrimidine nucleotides present in the antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and any purine nucleotides present in the antisense strand are 2'-deoxy purine nucleotides. In another embodiment, the antisense strand comprises one or more 2'-deoxy-2'-fluoro pyrimidine nucleotides and one or more 2'-O-methyl purine nucleotides. In another embodiment, the pyrimidine nucleotides present in the antisense strand are 2'-deoxy-2'-fluoro pyrimidine nucleotides and any purine nucleotides present in the antisense strand are 2'-O-methyl purine nucleotides. In a further embodiment the sense strand comprises a 3'-end and a 5'-end, wherein a terminal cap moiety (e.g., an inverted deoxy abasic moiety or inverted deoxy nucleotide moiety such as inverted thymidine) is present at the 5'-end, the 3'-end, or both of the 5' and 3' ends of the sense strand. In another embodiment, the antisense strand comprises a phosphorothioate internucleotide linkage at the 3' end of the antisense strand. In another embodiment, the antisense strand comprises a glyceryl modification at the 3' end. In another embodiment, the 5'-end of the antisense strand optionally includes a phosphate group.

In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a RE gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of RE RNA or a portion thereof, wherein the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, and wherein each of the two strands of the siNA molecule comprises about 21 nucleotides. In one embodiment, about 21

nucleotides of each strand of the siNA molecule are base-paired to the complementary nucleotides of the other strand of the siNA molecule. In another embodiment, about 19 nucleotides of each strand of the siNA molecule are base-paired to the complementary nucleotides of the other strand of the siNA molecule, wherein at least two 3' terminal
5 nucleotides of each strand of the siNA molecule are not base-paired to the nucleotides of the other strand of the siNA molecule. In another embodiment, each of the two 3' terminal nucleotides of each fragment of the siNA molecule is a 2'-deoxy-pyrimidine, such as 2'-deoxy-thymidine. In another embodiment, each strand of the siNA molecule is base-paired to the complementary nucleotides of the other strand of the siNA molecule.
10 In another embodiment, about 19 nucleotides of the antisense strand are base-paired to the nucleotide sequence of the RE RNA or a portion thereof. In another embodiment, about 21 nucleotides of the antisense strand are base-paired to the nucleotide sequence of the RE RNA or a portion thereof.

In one embodiment, the invention features a double-stranded short interfering
15 nucleic acid (siNA) molecule that inhibits expression of a RE gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of RE RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a
20 majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, and wherein the 5'-end of the antisense strand optionally includes a phosphate group.

In one embodiment, the invention features a double-stranded short interfering
nucleic acid (siNA) molecule that inhibits expression of a RE gene, wherein one of the
25 strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of RE RNA or a portion thereof, the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand and wherein a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule
30 comprises a sugar modification, and wherein the nucleotide sequence or a portion thereof

of the antisense strand is complementary to a nucleotide sequence of the untranslated region or a portion thereof of the RE RNA.

5 In one embodiment, the invention features a double-stranded short interfering nucleic acid (siNA) molecule that inhibits expression of a RE gene, wherein one of the strands of the double-stranded siNA molecule is an antisense strand which comprises nucleotide sequence that is complementary to nucleotide sequence of RE RNA or a portion thereof, wherein the other strand is a sense strand which comprises nucleotide sequence that is complementary to a nucleotide sequence of the antisense strand, wherein
10 a majority of the pyrimidine nucleotides present in the double-stranded siNA molecule comprises a sugar modification, and wherein the nucleotide sequence of the antisense strand is complementary to a nucleotide sequence of the RE RNA or a portion thereof that is present in the RE RNA.

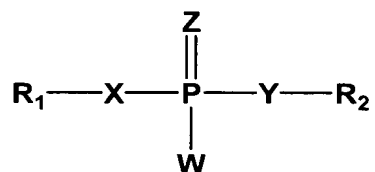
In one embodiment, the invention features a composition comprising a siNA molecule of the invention in a pharmaceutically acceptable carrier or diluent.

15 In a non-limiting example, the introduction of chemically-modified nucleotides into nucleic acid molecules provides a powerful tool in overcoming potential limitations of *in vivo* stability and bioavailability inherent to native RNA molecules that are delivered exogenously. For example, the use of chemically-modified nucleic acid molecules can enable a lower dose of a particular nucleic acid molecule for a given
20 therapeutic effect since chemically-modified nucleic acid molecules tend to have a longer half-life in serum. Furthermore, certain chemical modifications can improve the bioavailability of nucleic acid molecules by targeting particular cells or tissues and/or improving cellular uptake of the nucleic acid molecule. Therefore, even if the activity of a chemically-modified nucleic acid molecule is reduced as compared to a native nucleic
25 acid molecule, for example, when compared to an all-RNA nucleic acid molecule, the overall activity of the modified nucleic acid molecule can be greater than that of the native molecule due to improved stability and/or delivery of the molecule. Unlike native unmodified siNA, chemically-modified siNA can also minimize the possibility of activating interferon activity in humans.

In any of the embodiments of siNA molecules described herein, the antisense region of a siNA molecule of the invention can comprise a phosphorothioate internucleotide linkage at the 3'-end of said antisense region. In any of the embodiments of siNA molecules described herein, the antisense region can comprise about one to
5 about five phosphorothioate internucleotide linkages at the 5'-end of said antisense region. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs of a siNA molecule of the invention can comprise ribonucleotides or deoxyribonucleotides that are chemically-modified at a nucleic acid sugar, base, or backbone. In any of the embodiments of siNA molecules described herein, the 3'-
10 terminal nucleotide overhangs can comprise one or more universal base ribonucleotides. In any of the embodiments of siNA molecules described herein, the 3'-terminal nucleotide overhangs can comprise one or more acyclic nucleotides.

One embodiment of the invention provides an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention in a manner
15 that allows expression of the nucleic acid molecule. Another embodiment of the invention provides a mammalian cell comprising such an expression vector. The mammalian cell can be a human cell. The siNA molecule of the expression vector can comprise a sense region and an antisense region. The antisense region can comprise sequence complementary to a RNA or DNA sequence encoding RE and the sense region
20 can comprise sequence complementary to the antisense region. The siNA molecule can comprise two distinct strands having complementary sense and antisense regions. The siNA molecule can comprise a single strand having complementary sense and antisense regions.

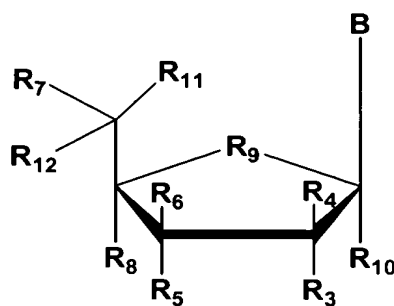
In one embodiment, the invention features a chemically-modified short interfering
25 nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a RE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides comprising a backbone modified internucleotide linkage having Formula I:



wherein each R1 and R2 is independently any nucleotide, non-nucleotide, or polynucleotide which can be naturally-occurring or chemically-modified, each X and Y is independently O, S, N, alkyl, or substituted alkyl, each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, or acetyl and wherein W, X, Y, and Z are optionally not all O. In another embodiment, a backbone modification of the invention comprises a phosphonoacetate and/or thiophosphonoacetate internucleotide linkage (see for example Sheehan et al., 2003, Nucleic Acids Research, 31, 4109-4118).

The chemically-modified internucleotide linkages having Formula I, for example, wherein any Z, W, X, and/or Y independently comprises a sulphur atom, can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) chemically-modified internucleotide linkages having Formula I at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified internucleotide linkages having Formula I at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In yet another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine nucleotides with chemically-modified internucleotide linkages having Formula I in the sense strand, the antisense strand, or both strands. In another embodiment, a siNA molecule of the invention having internucleotide linkage(s) of Formula I also comprises a chemically-modified nucleotide or non-nucleotide having any of Formulae I-VII.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a RE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula II:

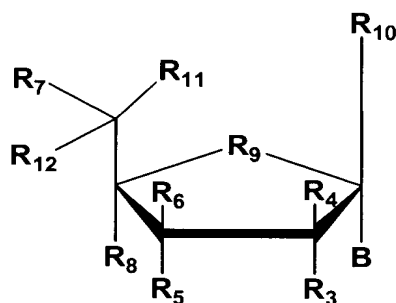


wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF₃, OCF₃, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R9 is O, S, CH₂, S=O, CHF, or CF₂, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula II can be present in one or both oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula II at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can

comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotides or non-nucleotides of Formula II at the 3'-end of the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a RE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) nucleotides or non-nucleotides having Formula III:

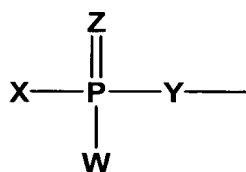


wherein each R3, R4, R5, R6, R7, R8, R10, R11 and R12 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF₃, OCF₃, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R9 is O, S, CH₂, S=O, CHF, or CF₂, and B is a nucleosidic base such as adenine, guanine, uracil, cytosine, thymine, 2-aminoadenosine, 5-methylcytosine, 2,6-diaminopurine, or any other non-naturally occurring base that can be employed to be complementary or non-complementary to target RNA or a non-nucleosidic base such as phenyl, naphthyl, 3-nitropyrrole, 5-nitroindole, nebularine, pyridone, pyridinone, or any other non-naturally occurring universal base that can be complementary or non-complementary to target RNA.

The chemically-modified nucleotide or non-nucleotide of Formula III can be present in one or both oligonucleotide strands of the siNA duplex, for example, in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide(s) or non-nucleotide(s) of Formula III at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*, about 1, 2, 3, 4, 5, or more) chemically-modified nucleotide or non-nucleotide of Formula III at the 3'-end of the sense strand, the antisense strand, or both strands.

In another embodiment, a siNA molecule of the invention comprises a nucleotide having Formula II or III, wherein the nucleotide having Formula II or III is in an inverted configuration. For example, the nucleotide having Formula II or III is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a RE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a 5'-terminal phosphate group having Formula IV:



wherein each X and Y is independently O, S, N, alkyl, substituted alkyl, or alkylhalo; wherein each Z and W is independently O, S, N, alkyl, substituted alkyl, O-alkyl, S-alkyl, alkaryl, aralkyl, alkylhalo, or acetyl; and wherein W, X, Y and Z are not all O.

In one embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand, for example, a

strand complementary to a target RNA, wherein the siNA molecule comprises an all RNA siNA molecule. In another embodiment, the invention features a siNA molecule having a 5'-terminal phosphate group having Formula IV on the target-complementary strand wherein the siNA molecule also comprises about 1 to about 3 (*e.g.*, about 1, 2, or 3) nucleotide 3'-terminal nucleotide overhangs having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) deoxyribonucleotides on the 3'-end of one or both strands. In another embodiment, a 5'-terminal phosphate group having Formula IV is present on the target-complementary strand of a siNA molecule of the invention, for example a siNA molecule having chemical modifications having any of Formulae I-VII.

10 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) against a RE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises one or more phosphorothioate internucleotide linkages. For example, in a non-limiting example, the invention features a chemically-modified short interfering
15 nucleic acid (siNA) having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in one siNA strand. In yet another embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) individually having about 1, 2, 3, 4, 5, 6, 7, 8 or more phosphorothioate internucleotide linkages in both siNA strands. The phosphorothioate internucleotide linkages can be present in one or both
20 oligonucleotide strands of the siNA duplex, for example in the sense strand, the antisense strand, or both strands. The siNA molecules of the invention can comprise one or more phosphorothioate internucleotide linkages at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand, the antisense strand, or both strands. For example, an exemplary siNA molecule of the invention can comprise about 1 to about 5 or more (*e.g.*,
25 about 1, 2, 3, 4, 5, or more) consecutive phosphorothioate internucleotide linkages at the 5'-end of the sense strand, the antisense strand, or both strands. In another non-limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) pyrimidine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands. In yet another non-
30 limiting example, an exemplary siNA molecule of the invention can comprise one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) purine phosphorothioate internucleotide linkages in the sense strand, the antisense strand, or both strands.

In one embodiment, the invention features a siNA molecule, wherein the sense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the sense strand comprises about 1 to about 5, specifically about 1, 2, 3, 4, or 5 phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more, pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro

nucleotides, with or without about 1 to about 5 or more, for example about 1, 2, 3, 4, 5, or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

5 In one embodiment, the invention features a siNA molecule, wherein the antisense strand comprises one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more phosphorothioate internucleotide linkages, and/or about one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and
 10 optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 10 or more, specifically about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3,
 15 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides,
 20 with or without one or more, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3' and 5'-ends, being present in the same or different strand.

In another embodiment, the invention features a siNA molecule, wherein the antisense strand comprises about 1 to about 5 or more, specifically about 1, 2, 3, 4, 5 or
 25 more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl, 2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the sense strand; and wherein the antisense strand comprises about 1 to about 5 or
 30 more, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) 2'-deoxy, 2'-O-methyl,

2'-deoxy-2'-fluoro, and/or one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more) universal base modified nucleotides, and optionally a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of the antisense strand. In another embodiment, one or more, for example about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more pyrimidine nucleotides of the sense and/or antisense siNA strand are chemically-modified with 2'-deoxy, 2'-O-methyl and/or 2'-deoxy-2'-fluoro nucleotides, with or without about 1 to about 5, for example about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages and/or a terminal cap molecule at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends, being present in the same or different strand.

10 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule having about 1 to about 5, specifically about 1, 2, 3, 4, 5 or more phosphorothioate internucleotide linkages in each strand of the siNA molecule.

In another embodiment, the invention features a siNA molecule comprising 2'-5' internucleotide linkages. The 2'-5' internucleotide linkage(s) can be at the 3'-end, the 5'-end, or both of the 3'- and 5'-ends of one or both siNA sequence strands. In addition, the 2'-5' internucleotide linkage(s) can be present at various other positions within one or both siNA sequence strands, for example, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a pyrimidine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage, or about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more including every internucleotide linkage of a purine nucleotide in one or both strands of the siNA molecule can comprise a 2'-5' internucleotide linkage.

In another embodiment, a chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified, wherein each strand is about 18 to about 27 (*e.g.*, about 18, 19, 20, 21, 22, 23, 24, 25, 26, or 27) nucleotides in length, wherein the duplex has about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the chemical modification comprises a structure having any of Formulae I-VII. For example, an exemplary chemically-modified siNA molecule of the invention comprises a duplex having two strands, one or both of which can be chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein each strand consists of about 21 nucleotides, each having a 2-nucleotide 3'-terminal nucleotide overhang, and

wherein the duplex has about 19 base pairs. In another embodiment, a siNA molecule of the invention comprises a single stranded hairpin structure, wherein the siNA is about 36 to about 70 (*e.g.*, about 36, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 19 base pairs and a 2-nucleotide 3'-terminal nucleotide overhang. In another embodiment, a linear hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. For example, a linear hairpin siNA molecule of the invention is designed such that degradation of the loop portion of the siNA molecule *in vivo* can generate a double-stranded siNA molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In another embodiment, a siNA molecule of the invention comprises a hairpin structure, wherein the siNA is about 25 to about 50 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides in length having about 3 to about 25 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) base pairs, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 25 to about 35 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35) nucleotides that is chemically-modified with one or more chemical modifications having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms a hairpin structure having about 3 to about 23 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or 23) base pairs and a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV). In another embodiment, a linear hairpin siNA molecule of the invention contains a stem

loop motif, wherein the loop portion of the siNA molecule is biodegradable. In another embodiment, a linear hairpin siNA molecule of the invention comprises a loop portion comprising a non-nucleotide linker.

In another embodiment, a siNA molecule of the invention comprises an asymmetric hairpin structure, wherein the siNA is about 25 to about 50 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides in length having about 3 to about 20 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) base pairs, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises a linear oligonucleotide having about 25 to about 35 (*e.g.*, about 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, or 35) nucleotides that is chemically-modified with one or more chemical modifications having any of Formulae I-VII or any combination thereof, wherein the linear oligonucleotide forms an asymmetric hairpin structure having about 3 to about 18 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or 18) base pairs and a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV). In another embodiment, an asymmetric hairpin siNA molecule of the invention contains a stem loop motif, wherein the loop portion of the siNA molecule is biodegradable. In another embodiment, an asymmetric hairpin siNA molecule of the invention comprises a loop portion comprising a non-nucleotide linker.

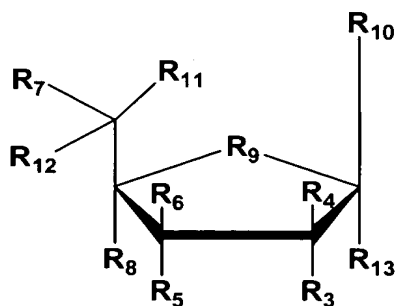
In another embodiment, a siNA molecule of the invention comprises an asymmetric double stranded structure having separate polynucleotide strands comprising sense and antisense regions, wherein the antisense region is about 16 to about 25 (*e.g.*, about 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25) nucleotides in length, wherein the sense region is about 3 to about 18 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) nucleotides in length, wherein the sense region and the antisense region have at least 3 complementary nucleotides, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of the invention comprises an asymmetric double stranded structure having separate

polynucleotide strands comprising sense and antisense regions, wherein the antisense region is about 18 to about 22 (*e.g.*, about 18, 19, 20, 21, or 22) nucleotides in length and wherein the sense region is about 3 to about 15 (*e.g.*, about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15) nucleotides in length, wherein the sense region the antisense region have at least 3 complementary nucleotides, and wherein the siNA can include one or more chemical modifications comprising a structure having any of Formulae I-VII or any combination thereof. In another embodiment, the asymmetric double stranded siNA molecule can also have a 5'-terminal phosphate group that can be chemically modified as described herein (for example a 5'-terminal phosphate group having Formula IV).

10 In another embodiment, a siNA molecule of the invention comprises a circular nucleic acid molecule, wherein the siNA is about 38 to about 70 (*e.g.*, about 38, 40, 45, 50, 55, 60, 65, or 70) nucleotides in length having about 18 to about 23 (*e.g.*, about 18, 19, 20, 21, 22, or 23) base pairs, and wherein the siNA can include a chemical modification, which comprises a structure having any of Formulae I-VII or any combination thereof. For example, an exemplary chemically-modified siNA molecule of
15 the invention comprises a circular oligonucleotide having about 42 to about 50 (*e.g.*, about 42, 43, 44, 45, 46, 47, 48, 49, or 50) nucleotides that is chemically-modified with a chemical modification having any of Formulae I-VII or any combination thereof, wherein the circular oligonucleotide forms a dumbbell shaped structure having about 19
20 base pairs and 2 loops.

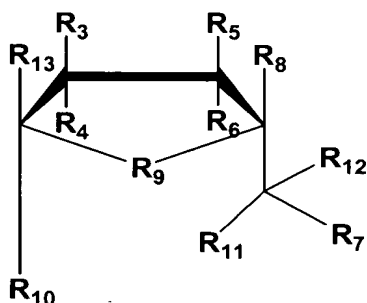
In another embodiment, a circular siNA molecule of the invention contains two loop motifs, wherein one or both loop portions of the siNA molecule is biodegradable. For example, a circular siNA molecule of the invention is designed such that degradation of the loop portions of the siNA molecule *in vivo* can generate a double-stranded siNA
25 molecule with 3'-terminal overhangs, such as 3'-terminal nucleotide overhangs comprising about 2 nucleotides.

In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) abasic moiety, for example a compound having Formula V:



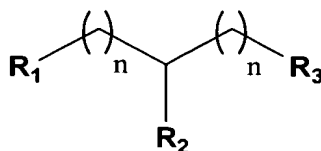
wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R9 is O, S, CH2, S=O, CHF, or CF2.

In one embodiment, a siNA molecule of the invention comprises at least one (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) inverted abasic moiety, for example a compound having Formula VI:



wherein each R3, R4, R5, R6, R7, R8, R10, R11, R12, and R13 is independently H, OH, alkyl, substituted alkyl, alkaryl or aralkyl, F, Cl, Br, CN, CF3, OCF3, OCN, O-alkyl, S-alkyl, N-alkyl, O-alkenyl, S-alkenyl, N-alkenyl, SO-alkyl, alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO2, NO2, N3, NH2, aminoalkyl, aminoacid, aminoacyl, ONH2, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or group having Formula I or II; R9 is O, S, CH2, S=O, CHF, or CF2,

5 example a compound having Formula VII:



10 alkyl-OSH, alkyl-OH, O-alkyl-OH, O-alkyl-SH, S-alkyl-OH, S-alkyl-SH, alkyl-S-alkyl, alkyl-O-alkyl, ONO₂, NO₂, N₃, NH₂, aminoalkyl, aminoacid, aminoacyl, ONH₂, O-aminoalkyl, O-aminoacid, O-aminoacyl, heterocycloalkyl, heterocycloalkaryl, aminoalkylamino, polyalkylamino, substituted silyl, or a group having Formula I, and R₁, R₂ or R₃ serves as points of attachment to the siNA molecule of the invention.

15 In another embodiment, the invention features a compound having Formula VII, wherein R1 and R2 are hydroxyl (OH) groups, n = 1, and R3 comprises O and is the point of attachment to the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both strands of a double-stranded siNA molecule of the invention or to a single-stranded siNA molecule of the invention. This modification is referred to herein as "glyceryl" (for
20 example modification 6 in **Figure 10**).

25 or both antisense and sense strands of the siNA molecule. In addition, a moiety having Formula VII can be present at the 3'-end or the 5'-end of a hairpin siNA molecule as described herein.

In another embodiment, a siNA molecule of the invention comprises an abasic residue having Formula V or VI, wherein the abasic residue having Formula VI or VI is connected to the siNA construct in a 3'-3', 3'-2', 2'-3', or 5'-5' configuration, such as at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of one or both siNA strands.

5 In one embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) locked nucleic acid (LNA) nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

10 In another embodiment, a siNA molecule of the invention comprises one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) acyclic nucleotides, for example at the 5'-end, the 3'-end, both of the 5' and 3'-ends, or any combination thereof, of the siNA molecule.

15 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*,
20 wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

25 In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*,
30 wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), wherein any nucleotides

comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any
5 (e.g., one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (e.g., one or more or all)
10 purine nucleotides present in the sense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising a sense region, wherein any
15 (e.g., one or more or all) pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), wherein any (e.g., one or more or all) purine
20 nucleotides present in the sense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said sense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein
25 any (e.g., one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (e.g., one or
30 more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and wherein any nucleotides comprising a 3'-terminal nucleotide overhang that are present in said antisense region are 2'-deoxy nucleotides.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention comprising an antisense region, wherein any (*e.g.*, one or more or all) pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any (*e.g.*, one or more or all) purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides).

In one embodiment, the invention features a chemically-modified short interfering nucleic acid (siNA) molecule of the invention capable of mediating RNA interference

(RNAi) against a RE inside a cell or reconstituted *in vitro* system comprising a sense region, wherein one or more pyrimidine nucleotides present in the sense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and one or more purine nucleotides present in the sense region are 2'-deoxy purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides), and an antisense region, wherein one or more pyrimidine nucleotides present in the antisense region are 2'-deoxy-2'-fluoro pyrimidine nucleotides (*e.g.*, wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and one or more purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). The sense region and/or the antisense region can have a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the sense and/or antisense sequence. The sense and/or antisense region can optionally further comprise a 3'-terminal nucleotide overhang having about 1 to about 4 (*e.g.*, about 1, 2, 3, or 4) 2'-deoxynucleotides. The overhang nucleotides can further comprise one or more (*e.g.*, about 1, 2, 3, 4 or more) phosphorothioate, phosphonoacetate, and/or thiophosphonoacetate internucleotide linkages. Non-limiting examples of these chemically-modified siNAs are shown in **Figures 4 and 5** and **Tables III and IV** herein. In any of these described embodiments, the purine nucleotides present in the sense region are alternatively 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides) and one or more purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (*e.g.*, wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). Also, in any of these embodiments, one or more purine nucleotides present in the sense region are alternatively purine ribonucleotides (*e.g.*, wherein all purine nucleotides are purine ribonucleotides or

alternately a plurality of purine nucleotides are purine ribonucleotides) and any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides). Additionally, in any of these embodiments, one or more purine nucleotides present in the sense region and/or present in the antisense region are alternatively selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides (e.g., wherein all purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides or alternately a plurality of purine nucleotides are selected from the group consisting of 2'-deoxy nucleotides, locked nucleic acid (LNA) nucleotides, 2'-methoxyethyl nucleotides, 4'-thionucleotides, and 2'-O-methyl nucleotides).

In another embodiment, any modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the siNA molecules of the invention, preferably in the antisense strand of the siNA molecules of the invention, but also optionally in the sense and/or both antisense and sense strands, are resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi. Non-limiting examples of nucleotides having a northern configuration include locked nucleic acid (LNA) nucleotides (e.g., 2'-O, 4'-C-methylene-(D-ribofuranosyl) nucleotides); 2'-methoxyethoxy (MOE) nucleotides; 2'-methyl-thio-ethyl, 2'-deoxy-2'-fluoro nucleotides, 2'-deoxy-2'-chloro nucleotides, 2'-azido nucleotides, and 2'-O-methyl nucleotides.

In one embodiment, the sense strand of a double stranded siNA molecule of the invention comprises a terminal cap moiety, (see for example **Figure 10**) such as an

inverted deoxyabaisc moiety, at the 3'-end, 5'-end, or both 3' and 5'-ends of the sense strand.

In one embodiment, the invention features a chemically-modified short interfering nucleic acid molecule (siNA) capable of mediating RNA interference (RNAi) against a
5 RE inside a cell or reconstituted *in vitro* system, wherein the chemical modification comprises a conjugate covalently attached to the chemically-modified siNA molecule. Non-limiting examples of conjugates contemplated by the invention include conjugates and ligands described in Vargeese *et al.*, USSN 10/427,160, filed April 30, 2003, incorporated by reference herein in its entirety, including the drawings. In another
10 embodiment, the conjugate is covalently attached to the chemically-modified siNA molecule via a biodegradable linker. In one embodiment, the conjugate molecule is attached at the 3'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule. In another embodiment, the conjugate molecule is attached at the 5'-end of either the sense strand, the antisense strand, or both
15 strands of the chemically-modified siNA molecule. In yet another embodiment, the conjugate molecule is attached both the 3'-end and 5'-end of either the sense strand, the antisense strand, or both strands of the chemically-modified siNA molecule, or any combination thereof. In one embodiment, a conjugate molecule of the invention comprises a molecule that facilitates delivery of a chemically-modified siNA molecule
20 into a biological system, such as a cell. In another embodiment, the conjugate molecule attached to the chemically-modified siNA molecule is a polyethylene glycol, human serum albumin, or a ligand for a cellular receptor that can mediate cellular uptake. Examples of specific conjugate molecules contemplated by the instant invention that can be attached to chemically-modified siNA molecules are described in Vargeese *et al.*,
25 U.S. Serial No. 10/201,394, incorporated by reference herein. The type of conjugates used and the extent of conjugation of siNA molecules of the invention can be evaluated for improved pharmacokinetic profiles, bioavailability, and/or stability of siNA constructs while at the same time maintaining the ability of the siNA to mediate RNAi activity. As such, one skilled in the art can screen siNA constructs that are modified
30 with various conjugates to determine whether the siNA conjugate complex possesses improved properties while maintaining the ability to mediate RNAi, for example in animal models as are generally known in the art.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule of the invention, wherein the siNA further comprises a nucleotide, non-nucleotide, or mixed nucleotide/non-nucleotide linker that joins the sense region of the siNA to the antisense region of the siNA. In one embodiment, a nucleotide linker of the invention can be a linker of ≥ 2 nucleotides in length, for example about 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides in length. In another embodiment, the nucleotide linker can be a nucleic acid aptamer. By "aptamer" or "nucleic acid aptamer" as used herein is meant a nucleic acid molecule that binds specifically to a target molecule wherein the nucleic acid molecule has sequence that comprises a sequence recognized by the target molecule in its natural setting. Alternately, an aptamer can be a nucleic acid molecule that binds to a target molecule where the target molecule does not naturally bind to a nucleic acid. The target molecule can be any molecule of interest. For example, the aptamer can be used to bind to a ligand-binding domain of a protein, thereby preventing interaction of the naturally occurring ligand with the protein. This is a non-limiting example and those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art. (See, for example, Gold *et al.*, 1995, *Annu. Rev. Biochem.*, 64, 763; Brody and Gold, 2000, *J. Biotechnol.*, 74, 5; Sun, 2000, *Curr. Opin. Mol. Ther.*, 2, 100; Kusser, 2000, *J. Biotechnol.*, 74, 27; Hermann and Patel, 2000, *Science*, 287, 820; and Jayasena, 1999, *Clinical Chemistry*, 45, 1628.)

In yet another embodiment, a non-nucleotide linker of the invention comprises a basic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, polyhydrocarbon, or other polymeric compounds (e.g. polyethylene glycols such as those having between 2 and 100 ethylene glycol units). Specific examples include those described by Seela and Kaiser, *Nucleic Acids Res.* 1990, 18:6353 and *Nucleic Acids Res.* 1987, 15:3113; Cload and Schepartz, *J. Am. Chem. Soc.* 1991, 113:6324; Richardson and Schepartz, *J. Am. Chem. Soc.* 1991, 113:5109; Ma *et al.*, *Nucleic Acids Res.* 1993, 21:2585 and *Biochemistry* 1993, 32:1751; Durand *et al.*, *Nucleic Acids Res.* 1990, 18:6353; McCurdy *et al.*, *Nucleosides & Nucleotides* 1991, 10:287; Jsckke *et al.*, *Tetrahedron Lett.* 1993, 34:301; Ono *et al.*, *Biochemistry* 1991, 30:9914; Arnold *et al.*, International Publication No. WO 89/02439; Usman *et al.*, International Publication No. WO 95/06731; Dudycz *et al.*, International Publication No. WO 95/11910 and Ferentz and Verdine, *J. Am. Chem. Soc.* 1991, 113:4000, all hereby incorporated by reference

herein. A "non-nucleotide" further means any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound can be abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine, for example at the C1 position of the sugar.

In one embodiment, the invention features a short interfering nucleic acid (siNA) molecule capable of mediating RNA interference (RNAi) inside a cell or reconstituted in vitro system, wherein one or both strands of the siNA molecule that are assembled from two separate oligonucleotides do not comprise any ribonucleotides. For example, a siNA molecule can be assembled from a single oligonucleotide where the sense and antisense regions of the siNA comprise separate oligonucleotides not having any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotides. In another example, a siNA molecule can be assembled from a single oligonucleotide where the sense and antisense regions of the siNA are linked or circularized by a nucleotide or non-nucleotide linker as described herein, wherein the oligonucleotide does not have any ribonucleotides (e.g., nucleotides having a 2'-OH group) present in the oligonucleotide. Applicant has surprisingly found that the presense of ribonucleotides (e.g., nucleotides having a 2'-hydroxyl group) within the siNA molecule is not required or essential to support RNAi activity. As such, in one embodiment, all positions within the siNA can include chemically modified nucleotides and/or non-nucleotides such as nucleotides and or non-nucleotides having Formula I, II, III, IV, V, VI, or VII or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system comprising a single stranded polynucleotide having complementarity to a target nucleic acid sequence. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group. In another embodiment, the single stranded siNA molecule of the invention comprises a 5'-terminal phosphate group and a 3'-terminal phosphate group (e.g., a 2',3'-cyclic phosphate). In another embodiment, the

single stranded siNA molecule of the invention comprises about 19 to about 29 (e.g., about 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29) nucleotides. In yet another embodiment, the single stranded siNA molecule of the invention comprises one or more chemically modified nucleotides or non-nucleotides described herein. For example, all the positions within the siNA molecule can include chemically-modified nucleotides such as nucleotides having any of Formulae I-VII, or any combination thereof to the extent that the ability of the siNA molecule to support RNAi activity in a cell is maintained.

In one embodiment, a siNA molecule of the invention is a single stranded siNA molecule that mediates RNAi activity in a cell or reconstituted in vitro system comprising a single stranded polynucleotide having complementarity to a target nucleic acid sequence, wherein one or more pyrimidine nucleotides present in the siNA are 2'-deoxy-2'-fluoro pyrimidine nucleotides (e.g., wherein all pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides or alternately a plurality of pyrimidine nucleotides are 2'-deoxy-2'-fluoro pyrimidine nucleotides), and wherein any purine nucleotides present in the antisense region are 2'-O-methyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-O-methyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-O-methyl purine nucleotides), and a terminal cap modification, such as any modification described herein or shown in **Figure 10**, that is optionally present at the 3'-end, the 5'-end, or both of the 3' and 5'-ends of the antisense sequence. The siNA optionally further comprises about 1 to about 4 or more (e.g., about 1, 2, 3, 4 or more) terminal 2'-deoxynucleotides at the 3'-end of the siNA molecule, wherein the terminal nucleotides can further comprise one or more (e.g., 1, 2, 3, 4 or more) phosphorothioate, phosphonoacetate, and/or thiophosphonoacetate internucleotide linkages, and wherein the siNA optionally further comprises a terminal phosphate group, such as a 5'-terminal phosphate group. In any of these embodiments, any purine nucleotides present in the antisense region are alternatively 2'-deoxy purine nucleotides (e.g., wherein all purine nucleotides are 2'-deoxy purine nucleotides or alternately a plurality of purine nucleotides are 2'-deoxy purine nucleotides). Also, in any of these embodiments, any purine nucleotides present in the siNA (i.e., purine nucleotides present in the sense and/or antisense region) can alternatively be locked nucleic acid (LNA) nucleotides (e.g., wherein all purine nucleotides are LNA nucleotides or alternately a plurality of purine

nucleotides are LNA nucleotides). Also, in any of these embodiments, any purine nucleotides present in the siNA are alternatively 2'-methoxyethyl purine nucleotides (e.g., wherein all purine nucleotides are 2'-methoxyethyl purine nucleotides or alternately a plurality of purine nucleotides are 2'-methoxyethyl purine nucleotides). In
5 another embodiment, any modified nucleotides present in the single stranded siNA molecules of the invention comprise modified nucleotides having properties or characteristics similar to naturally occurring ribonucleotides. For example, the invention features siNA molecules including modified nucleotides having a Northern conformation (e.g., Northern pseudorotation cycle, see for example Saenger, *Principles of Nucleic Acid*
10 *Structure*, Springer-Verlag ed., 1984). As such, chemically modified nucleotides present in the single stranded siNA molecules of the invention are preferably resistant to nuclease degradation while at the same time maintaining the capacity to mediate RNAi.

In one embodiment, the invention features a method for modulating the expression of a RE gene within a cell comprising: (a) synthesizing a siNA molecule of the
15 invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the RE gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the RE gene in the cell.

In one embodiment, the invention features a method for modulating the expression
20 of a RE gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the RE gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequence of the target RNA; and (b) introducing the siNA molecule into a cell under
25 conditions suitable to modulate the expression of the RE gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one RE gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the RE genes; and (b)
30 introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the RE genes in the cell.

In another embodiment, the invention features a method for modulating the expression of two or more RE genes within a cell comprising: (a) synthesizing one or more siNA molecules of the invention, which can be chemically-modified, wherein the siNA strands comprise sequences complementary to RNA of the RE genes and wherein the sense strand sequences of the siNAs comprise sequences identical or substantially similar to the sequences of the target RNAs; and (b) introducing the siNA molecules into a cell under conditions suitable to modulate the expression of the RE genes in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one RE gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the RE gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequences of the target RNAs; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the RE genes in the cell.

In one embodiment, siNA molecules of the invention are used as reagents in ex vivo applications. For example, siNA reagents are introduced into tissue or cells that are transplanted into a subject for therapeutic effect. The cells and/or tissue can be derived from an organism or subject that later receives the explant, or can be derived from another organism or subject prior to transplantation. The siNA molecules can be used to modulate the expression of one or more genes in the cells or tissue, such that the cells or tissue obtain a desired phenotype or are able to perform a function when transplanted in vivo. In one embodiment, certain target cells from a patient are extracted. These extracted cells are contacted with siNAs targeting a specific nucleotide sequence within the cells under conditions suitable for uptake of the siNAs by these cells (e.g. using delivery reagents such as cationic lipids, liposomes and the like or using techniques such as electroporation to facilitate the delivery of siNAs into cells). The cells are then reintroduced back into the same patient or other patients. In one embodiment, the invention features a method of modulating the expression of a RE gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the RE gene; and (b) introducing the siNA molecule into a

cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the RE gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the RE gene in that organism.

In one embodiment, the invention features a method of modulating the expression of a RE gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the RE gene and wherein the sense strand sequence of the siNA comprises a sequence identical or substantially similar to the sequence of the target RNA; and (b) introducing the siNA molecule into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the RE gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the RE gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one RE gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the RE genes; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the RE genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the RE genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a RE gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the RE gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of

the RE gene in the organism. The level of RE protein or RNA can be determined as is known in the art.

5 In another embodiment, the invention features a method of modulating the expression of more than one RE gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein one of the siNA strands comprises a sequence complementary to RNA of the RE genes; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the RE genes in the organism. The level of RE protein or RNA can be determined as is known in the art.

10 In one embodiment, the invention features a method for modulating the expression of a RE gene within a cell comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the RE gene; and (b) introducing the siNA molecule into a cell under conditions suitable to modulate the expression of the
15 RE gene in the cell.

In another embodiment, the invention features a method for modulating the expression of more than one RE gene within a cell comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the RE gene;
20 and (b) contacting the cell in vitro or in vivo with the siNA molecule under conditions suitable to modulate the expression of the RE genes in the cell.

In one embodiment, the invention features a method of modulating the expression of a RE gene in a tissue explant comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single
25 stranded sequence having complementarity to RNA of the RE gene; and (b) contacting the cell of the tissue explant derived from a particular organism with the siNA molecule under conditions suitable to modulate the expression of the RE gene in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions
30 suitable to modulate the expression of the RE gene in that organism.

In another embodiment, the invention features a method of modulating the expression of more than one RE gene in a tissue explant comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the RE gene; and (b) introducing the siNA molecules into a cell of the tissue explant derived from a particular organism under conditions suitable to modulate the expression of the RE genes in the tissue explant. In another embodiment, the method further comprises introducing the tissue explant back into the organism the tissue was derived from or into another organism under conditions suitable to modulate the expression of the RE genes in that organism.

In one embodiment, the invention features a method of modulating the expression of a RE gene in an organism comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the RE gene; and (b) introducing the siNA molecule into the organism under conditions suitable to modulate the expression of the RE gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one RE gene in an organism comprising: (a) synthesizing siNA molecules of the invention, which can be chemically-modified, wherein the siNA comprises a single stranded sequence having complementarity to RNA of the RE gene; and (b) introducing the siNA molecules into the organism under conditions suitable to modulate the expression of the RE genes in the organism.

In one embodiment, the invention features a method of modulating the expression of a RE gene in an organism comprising contacting the organism with a siNA molecule of the invention under conditions suitable to modulate the expression of the RE gene in the organism.

In another embodiment, the invention features a method of modulating the expression of more than one RE gene in an organism comprising contacting the organism with one or more siNA molecules of the invention under conditions suitable to modulate the expression of the RE genes in the organism.

The siNA molecules of the invention can be designed to down regulate or inhibit target (RE) gene expression through RNAi targeting of a variety of RNA molecules. In one embodiment, the siNA molecules of the invention are used to target various RNAs corresponding to a target gene. Non-limiting examples of such RNAs include messenger RNA (mRNA), alternate RNA splice variants of target gene(s), post-transcriptionally modified RNA of target gene(s), pre-mRNA of target gene(s), and/or RNA templates. If alternate splicing produces a family of transcripts that are distinguished by usage of appropriate exons, the instant invention can be used to inhibit gene expression through the appropriate exons to specifically inhibit or to distinguish among the functions of gene family members. For example, a protein that contains an alternatively spliced transmembrane domain can be expressed in both membrane bound and secreted forms. Use of the invention to target the exon containing the transmembrane domain can be used to determine the functional consequences of pharmaceutical targeting of membrane bound as opposed to the secreted form of the protein. Non-limiting examples of applications of the invention relating to targeting these RNA molecules include therapeutic pharmaceutical applications, pharmaceutical discovery applications, molecular diagnostic and gene function applications, and gene mapping, for example using single nucleotide polymorphism mapping with siNA molecules of the invention. Such applications can be implemented using known gene sequences or from partial sequences available from an expressed sequence tag (EST).

In another embodiment, the siNA molecules of the invention are used to target conserved sequences corresponding to a gene family or gene families such as RE family genes. As such, siNA molecules targeting multiple RE targets can provide increased therapeutic effect. In addition, siNA can be used to characterize pathways of gene function in a variety of applications. For example, the present invention can be used to inhibit the activity of target gene(s) in a pathway to determine the function of uncharacterized gene(s) in gene function analysis, mRNA function analysis, or translational analysis. The invention can be used to determine potential target gene pathways involved in various diseases and conditions toward pharmaceutical development. The invention can be used to understand pathways of gene expression involved in, for example, the progression and/or maintenance of cancer.

In one embodiment, siNA molecule(s) and/or methods of the invention are used to down regulate the expression of gene(s) that encode RNA referred to by Genbank Accession, for example RE genes encoding RNA sequence(s) referred to herein by Genbank Accession number, for example, Genbank Accession Nos. shown in **Table I**.

5 In one embodiment, the invention features a method comprising: (a) generating a library of siNA constructs having a predetermined complexity; and (b) assaying the siNA constructs of (a) above, under conditions suitable to determine RNAi target sites within the target RNA sequence. In one embodiment, the siNA molecules of (a) have strands of a fixed length, for example, about 23 nucleotides in length. In another embodiment, the
10 siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. In another embodiment, fragments of target RNA are analyzed
15 for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

20 In one embodiment, the invention features a method comprising: (a) generating a randomized library of siNA constructs having a predetermined complexity, such as of 4^N , where N represents the number of base paired nucleotides in each of the siNA construct strands (*eg.* for a siNA construct having 21 nucleotide sense and antisense strands with 19 base pairs, the complexity would be 4^{19}); and (b) assaying the siNA constructs of (a)
25 above, under conditions suitable to determine RNAi target sites within the target RE RNA sequence. In another embodiment, the siNA molecules of (a) have strands of a fixed length, for example about 23 nucleotides in length. In yet another embodiment, the siNA molecules of (a) are of differing length, for example having strands of about 19 to about 25 (*e.g.*, about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one
30 embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described in Example 7 herein. In another embodiment, the assay can comprise a cell culture system

in which target RNA is expressed. In another embodiment, fragments of RE RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RE RNA sequence. The target RE RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by cellular expression in *in vivo* systems.

In another embodiment, the invention features a method comprising: (a) analyzing the sequence of a RNA target encoded by a target gene; (b) synthesizing one or more sets of siNA molecules having sequence complementary to one or more regions of the RNA of (a); and (c) assaying the siNA molecules of (b) under conditions suitable to determine RNAi targets within the target RNA sequence. In one embodiment, the siNA molecules of (b) have strands of a fixed length, for example about 23 nucleotides in length. In another embodiment, the siNA molecules of (b) are of differing length, for example having strands of about 19 to about 25 (e.g., about 19, 20, 21, 22, 23, 24, or 25) nucleotides in length. In one embodiment, the assay can comprise a reconstituted *in vitro* siNA assay as described herein. In another embodiment, the assay can comprise a cell culture system in which target RNA is expressed. Fragments of target RNA are analyzed for detectable levels of cleavage, for example by gel electrophoresis, northern blot analysis, or RNase protection assays, to determine the most suitable target site(s) within the target RNA sequence. The target RNA sequence can be obtained as is known in the art, for example, by cloning and/or transcription for *in vitro* systems, and by expression in *in vivo* systems.

By "target site" is meant a sequence within a target RNA that is "targeted" for cleavage mediated by a siNA construct which contains sequences within its antisense region that are complementary to the target sequence.

By "detectable level of cleavage" is meant cleavage of target RNA (and formation of cleaved product RNAs) to an extent sufficient to discern cleavage products above the background of RNAs produced by random degradation of the target RNA. Production of cleavage products from 1-5% of the target RNA is sufficient to detect above the background for most methods of detection.

In one embodiment, the invention features a composition comprising a siNA molecule of the invention, which can be chemically-modified, in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a pharmaceutical composition comprising siNA molecules of the invention, which can be chemically-modified, targeting one or more genes in a pharmaceutically acceptable carrier or diluent. In another embodiment, the invention features a method for diagnosing a disease or condition in a subject comprising administering to the subject a composition of the invention under conditions suitable for the diagnosis of the disease or condition in the subject. In another embodiment, the invention features a method for treating or preventing a disease or condition in a subject, comprising administering to the subject a composition of the invention under conditions suitable for the treatment or prevention of the disease or condition in the subject, alone or in conjunction with one or more other therapeutic compounds. In yet another embodiment, the invention features a method for reducing or preventing tissue rejection in a subject comprising administering to the subject a composition of the invention under conditions suitable for the reduction or prevention of tissue rejection in the subject.

In another embodiment, the invention features a method for validating a RE gene target, comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of a RE target gene; (b) introducing the siNA molecule into a cell, tissue, or organism under conditions suitable for modulating expression of the RE target gene in the cell, tissue, or organism; and (c) determining the function of the gene by assaying for any phenotypic change in the cell, tissue, or organism.

In another embodiment, the invention features a method for validating a RE target comprising: (a) synthesizing a siNA molecule of the invention, which can be chemically-modified, wherein one of the siNA strands includes a sequence complementary to RNA of a RE target gene; (b) introducing the siNA molecule into a biological system under conditions suitable for modulating expression of the RE target gene in the biological system; and (c) determining the function of the gene by assaying for any phenotypic change in the biological system.

By "biological system" is meant, material, in a purified or unpurified form, from biological sources, including but not limited to human or animal, wherein the system comprises the components required for RNAi activity. The term "biological system" includes, for example, a cell, tissue, or organism, or extract thereof. The term biological system also includes reconstituted RNAi systems that can be used in an *in vitro* setting.

By "phenotypic change" is meant any detectable change to a cell that occurs in response to contact or treatment with a nucleic acid molecule of the invention (e.g., siNA). Such detectable changes include, but are not limited to, changes in shape, size, proliferation, motility, protein expression or RNA expression or other physical or chemical changes as can be assayed by methods known in the art. The detectable change can also include expression of reporter genes/molecules such as Green Florescent Protein (GFP) or various tags that are used to identify an expressed protein or any other cellular component that can be assayed.

In one embodiment, the invention features a kit containing a siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of a RE target gene in a biological system, including, for example, in a cell, tissue, or organism. In another embodiment, the invention features a kit containing more than one siNA molecule of the invention, which can be chemically-modified, that can be used to modulate the expression of more than one RE target gene in a biological system, including, for example, in a cell, tissue, or organism.

In one embodiment, the invention features a cell containing one or more siNA molecules of the invention, which can be chemically-modified. In another embodiment, the cell containing a siNA molecule of the invention is a mammalian cell. In yet another embodiment, the cell containing a siNA molecule of the invention is a human cell.

In one embodiment, the synthesis of a siNA molecule of the invention, which can be chemically-modified, comprises: (a) synthesis of two complementary strands of the siNA molecule; (b) annealing the two complementary strands together under conditions suitable to obtain a double-stranded siNA molecule. In another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase oligonucleotide

synthesis. In yet another embodiment, synthesis of the two complementary strands of the siNA molecule is by solid phase tandem oligonucleotide synthesis.

In one embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing a first oligonucleotide sequence strand of the siNA molecule, wherein the first oligonucleotide sequence strand comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of the second oligonucleotide sequence strand of the siNA; (b) synthesizing the second oligonucleotide sequence strand of siNA on the scaffold of the first oligonucleotide sequence strand, wherein the second oligonucleotide sequence strand further comprises a chemical moiety than can be used to purify the siNA duplex; (c) cleaving the linker molecule of (a) under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex; and (d) purifying the siNA duplex utilizing the chemical moiety of the second oligonucleotide sequence strand. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions using an alkylamine base such as methylamine. In one embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place concomitantly. In another embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group, which can be employed in a trityl-on synthesis strategy as described herein. In yet another embodiment, the chemical moiety, such as a dimethoxytrityl group, is removed during purification, for example, using acidic conditions.

In a further embodiment, the method for siNA synthesis is a solution phase synthesis or hybrid phase synthesis wherein both strands of the siNA duplex are synthesized in tandem using a cleavable linker attached to the first sequence which acts a scaffold for synthesis of the second sequence. Cleavage of the linker under conditions

suitable for hybridization of the separate siNA sequence strands results in formation of the double-stranded siNA molecule.

In another embodiment, the invention features a method for synthesizing a siNA duplex molecule comprising: (a) synthesizing one oligonucleotide sequence strand of the siNA molecule, wherein the sequence comprises a cleavable linker molecule that can be used as a scaffold for the synthesis of another oligonucleotide sequence; (b) synthesizing a second oligonucleotide sequence having complementarity to the first sequence strand on the scaffold of (a), wherein the second sequence comprises the other strand of the double-stranded siNA molecule and wherein the second sequence further comprises a chemical moiety than can be used to isolate the attached oligonucleotide sequence; (c) purifying the product of (b) utilizing the chemical moiety of the second oligonucleotide sequence strand under conditions suitable for isolating the full-length sequence comprising both siNA oligonucleotide strands connected by the cleavable linker and under conditions suitable for the two siNA oligonucleotide strands to hybridize and form a stable duplex. In one embodiment, cleavage of the linker molecule in (c) above takes place during deprotection of the oligonucleotide, for example under hydrolysis conditions. In another embodiment, cleavage of the linker molecule in (c) above takes place after deprotection of the oligonucleotide. In another embodiment, the method of synthesis comprises solid phase synthesis on a solid support such as controlled pore glass (CPG) or polystyrene, wherein the first sequence of (a) is synthesized on a cleavable linker, such as a succinyl linker, using the solid support as a scaffold. The cleavable linker in (a) used as a scaffold for synthesizing the second strand can comprise similar reactivity or differing reactivity as the solid support derivatized linker, such that cleavage of the solid support derivatized linker and the cleavable linker of (a) takes place either concomitantly or sequentially. In one embodiment, the chemical moiety of (b) that can be used to isolate the attached oligonucleotide sequence comprises a trityl group, for example a dimethoxytrityl group.

In another embodiment, the invention features a method for making a double-stranded siNA molecule in a single synthetic process comprising: (a) synthesizing an oligonucleotide having a first and a second sequence, wherein the first sequence is complementary to the second sequence, and the first oligonucleotide sequence is linked

to the second sequence via a cleavable linker, and wherein a terminal 5'-protecting group, for example, a 5'-O-dimethoxytrityl group (5'-O-DMT) remains on the oligonucleotide having the second sequence; (b) deprotecting the oligonucleotide whereby the deprotection results in the cleavage of the linker joining the two oligonucleotide sequences; and (c) purifying the product of (b) under conditions suitable for isolating the double-stranded siNA molecule, for example using a trityl-on synthesis strategy as described herein.

In another embodiment, the method of synthesis of siNA molecules of the invention comprises the teachings of Scaringe *et al.*, US Patent Nos. 5,889,136; 6,008,400; and 6,111,086, incorporated by reference herein in their entirety.

In one embodiment, the invention features siNA constructs that mediate RNAi against a RE, wherein the siNA construct comprises one or more chemical modifications, for example, one or more chemical modifications having any of Formulae I-VII or any combination thereof that increases the nuclease resistance of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules with increased nuclease resistance comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased nuclease resistance.

In one embodiment, the invention features siNA constructs that mediate RNAi against a RE, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the sense and antisense strands of the siNA construct.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the sense and antisense strands of the siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the sense and antisense strands of the siNA molecule.

In one embodiment, the invention features siNA constructs that mediate RNAi against a RE, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target RNA sequence within a cell.

5 In one embodiment, the invention features siNA constructs that mediate RNAi against a RE, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the binding affinity between the antisense strand of the siNA construct and a complementary target DNA sequence within a cell.

10 In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target RNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand
15 of the siNA molecule and a complementary target RNA sequence.

In another embodiment, the invention features a method for generating siNA molecules with increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA
20 molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having increased binding affinity between the antisense strand of the siNA molecule and a complementary target DNA sequence.

In one embodiment, the invention features siNA constructs that mediate RNAi against a RE, wherein the siNA construct comprises one or more chemical modifications
25 described herein that modulate the polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA construct.

In another embodiment, the invention features a method for generating siNA molecules capable of mediating increased polymerase activity of a cellular polymerase

capable of generating additional endogenous siNA molecules having sequence homology to a chemically-modified siNA molecule comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules
5 capable of mediating increased polymerase activity of a cellular polymerase capable of generating additional endogenous siNA molecules having sequence homology to the chemically-modified siNA molecule.

In one embodiment, the invention features chemically-modified siNA constructs that mediate RNAi against a RE in a cell, wherein the chemical modifications do not
10 significantly effect the interaction of siNA with a target RNA molecule, DNA molecule and/or proteins or other factors that are essential for RNAi in a manner that would decrease the efficacy of RNAi mediated by such siNA constructs.

In another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against RE comprising (a) introducing
15 nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a RE target RNA comprising (a)
20 introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target RNA.

In yet another embodiment, the invention features a method for generating siNA molecules with improved RNAi activity against a RE target DNA comprising (a)
25 introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved RNAi activity against the target DNA.

In one embodiment, the invention features siNA constructs that mediate RNAi against a RE, wherein the siNA construct comprises one or more chemical modifications described herein that modulates the cellular uptake of the siNA construct.

5 In another embodiment, the invention features a method for generating siNA molecules against RE with improved cellular uptake comprising (a) introducing nucleotides having any of Formula I-VII or any combination thereof into a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved cellular uptake.

10 In one embodiment, the invention features siNA constructs that mediate RNAi against a RE, wherein the siNA construct comprises one or more chemical modifications described herein that increases the bioavailability of the siNA construct, for example, by attaching polymeric conjugates such as polyethyleneglycol or equivalent conjugates that improve the pharmacokinetics of the siNA construct, or by attaching conjugates that target specific tissue types or cell types *in vivo*. Non-limiting examples of such
15 conjugates are described in Vargeese *et al.*, U.S. Serial No. 10/201,394 incorporated by reference herein.

In one embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability, comprising (a) introducing a conjugate into the structure of a siNA molecule, and (b) assaying the siNA molecule of
20 step (a) under conditions suitable for isolating siNA molecules having improved bioavailability. Such conjugates can include ligands for cellular receptors, such as peptides derived from naturally occurring protein ligands; protein localization sequences, including cellular ZIP code sequences; antibodies; nucleic acid aptamers; vitamins and other co-factors, such as folate and N-acetylgalactosamine; polymers, such as
25 polyethyleneglycol (PEG); phospholipids; cholesterol; polyamines, such as spermine or spermidine; and others.

In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary to a target RNA sequence or a portion thereof, and a second sequence having
30 complementarity to said first sequence, wherein said second sequence is chemically

modified in a manner that it can no longer act as a guide sequence for efficiently mediating RNA interference and/or be recognized by cellular proteins that facilitate RNAi.

5 In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein the second sequence is designed or modified in a manner that prevents its entry into the RNAi pathway as a guide sequence or as a sequence that is complementary to a target nucleic acid (e.g., RNA) sequence.
10 Such design or modifications are expected to enhance the activity of siNA and/or improve the specificity of siNA molecules of the invention. These modifications are also expected to minimize any off-target effects and/or associated toxicity.

In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary
15 to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein said second sequence is incapable of acting as a guide sequence for mediating RNA interference.

In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary
20 to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein said second sequence does not have a terminal 5'-hydroxyl (5'-OH) or 5'-phosphate group.

In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary
25 to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein said second sequence comprises a terminal cap moiety at the 5'-end of said second sequence. In one embodiment, the terminal cap moiety comprises an inverted abasic, inverted deoxy abasic, inverted nucleotide moiety, a group shown in **Figure 10**, an alkyl or cycloalkyl group, a

heterocycle, or any other group that prevents RNAi activity in which the second sequence serves as a guide sequence or template for RNAi.

In one embodiment, the invention features a double stranded short interfering nucleic acid (siNA) molecule that comprises a first nucleotide sequence complementary to a target RNA sequence or a portion thereof, and a second sequence having complementarity to said first sequence, wherein said second sequence comprises a terminal cap moiety at the 5'-end and 3'-end of said second sequence. In one embodiment, each terminal cap moiety individually comprises an inverted abasic, inverted deoxy abasic, inverted nucleotide moiety, a group shown in **Figure 10**, an alkyl or cycloalkyl group, a heterocycle, or any other group that prevents RNAi activity in which the second sequence serves as a guide sequence or template for RNAi.

In one embodiment, the invention features a method for generating siNA molecules of the invention with improved specificity for down regulating or inhibiting the expression of a target nucleic acid (e.g., a DNA or RNA such as a gene or its corresponding RNA), comprising (a) introducing one or more chemical modifications into the structure of a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved specificity. In another embodiment, the chemical modification used to improve specificity comprises terminal cap modifications at the 5'-end, 3'-end, or both 5' and 3'-ends of the siNA molecule. The terminal cap modifications can comprise, for example, structures shown in **Figure 10** (e.g. inverted deoxyabasic moieties) or any other chemical modification that renders a portion of the siNA molecule (e.g. the sense strand) incapable of mediating RNA interference against an off target nucleic acid sequence. In a non-limiting example, a siNA molecule is designed such that only the antisense sequence of the siNA molecule can serve as a guide sequence for RISC mediated degradation of a corresponding target RNA sequence. This can be accomplished by rendering the sense sequence of the siNA inactive by introducing chemical modifications to the sense strand that preclude recognition of the sense strand as a guide sequence by RNAi machinery. In one embodiment, such chemical modifications comprise any chemical group at the 5'-end of the sense strand of the siNA, or any other group that serves to render the sense strand inactive as a guide sequence for mediating RNA interference. These modifications, for

example, can result in a molecule where the 5'-end of the sense strand no longer has a free 5'-hydroxyl (5'-OH) or a free 5'-phosphate group (e.g., phosphate, diphosphate, triphosphate, cyclic phosphate etc.). Non-limiting examples of such siNA constructs are described herein, such as "Stab 9/10", "Stab 7/8", "Stab 7/19" and "Stab 17/22"
5 chemistries and variants thereof wherein the 5'-end and 3'-end of the sense strand of the siNA do not comprise a hydroxyl group or phosphate group.

In one embodiment, the invention features a method for generating siNA molecules of the invention with improved specificity for down regulating or inhibiting the expression of a target nucleic acid (e.g., a DNA or RNA such as a gene or its
10 corresponding RNA), comprising introducing one or more chemical modifications into the structure of a siNA molecule that prevent a strand or portion of the siNA molecule from acting as a template or guide sequence for RNAi activity. In one embodiment, the inactive strand or sense region of the siNA molecule is the sense strand or sense region of the siNA molecule, i.e. the strand or region of the siNA that does not have
15 complementarity to the target nucleic acid sequence. In one embodiment, such chemical modifications comprise any chemical group at the 5'-end of the sense strand or region of the siNA that does not comprise a 5'-hydroxyl (5'-OH) or 5'-phosphate group, or any other group that serves to render the sense strand or sense region inactive as a guide sequence for mediating RNA interference. Non-limiting examples of such siNA
20 constructs are described herein, such as "Stab 9/10", "Stab 7/8", "Stab 7/19" and "Stab 17/22" chemistries and variants thereof wherein the 5'-end and 3'-end of the sense strand of the siNA do not comprise a hydroxyl group or phosphate group.

In one embodiment, the invention features a method for screening siNA molecules that are active in mediating RNA interference against a target nucleic acid sequence
25 comprising (a) generating a plurality of unmodified siNA molecules, (b) screening the siNA molecules of step (a) under conditions suitable for isolating siNA molecules that are active in mediating RNA interference against the target nucleic acid sequence, and (c) introducing chemical modifications (e.g. chemical modifications as described herein or as otherwise known in the art) into the active siNA molecules of (b). In one
30 embodiment, the method further comprises re-screening the chemically modified siNA molecules of step (c) under conditions suitable for isolating chemically modified siNA

molecules that are active in mediating RNA interference against the target nucleic acid sequence.

5 In one embodiment, the invention features a method for screening chemically modified siNA molecules that are active in mediating RNA interference against a target nucleic acid sequence comprising (a) generating a plurality of chemically modified siNA molecules (e.g. siNA molecules as described herein or as otherwise known in the art), and (b) screening the siNA molecules of step (a) under conditions suitable for isolating chemically modified siNA molecules that are active in mediating RNA interference against the target nucleic acid sequence.

10 The term “ligand” refers to any compound or molecule, such as a drug, peptide, hormone, or neurotransmitter, that is capable of interacting with another compound, such as a receptor, either directly or indirectly. The receptor that interacts with a ligand can be present on the surface of a cell or can alternately be an intercellular receptor. Interaction of the ligand with the receptor can result in a biochemical reaction, or can simply be a
15 physical interaction or association.

In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing an excipient formulation to a siNA molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.
20 Such excipients include polymers such as cyclodextrins, lipids, cationic lipids, polyamines, phospholipids, nanoparticles, receptors, ligands, and others.

In another embodiment, the invention features a method for generating siNA molecules of the invention with improved bioavailability comprising (a) introducing nucleotides having any of Formulae I-VII or any combination thereof into a siNA
25 molecule, and (b) assaying the siNA molecule of step (a) under conditions suitable for isolating siNA molecules having improved bioavailability.

In another embodiment, polyethylene glycol (PEG) can be covalently attached to siNA compounds of the present invention. The attached PEG can be any molecular weight, preferably from about 2,000 to about 50,000 daltons (Da).

The present invention can be used alone or as a component of a kit having at least one of the reagents necessary to carry out the *in vitro* or *in vivo* introduction of RNA to test samples and/or subjects. For example, preferred components of the kit include a siNA molecule of the invention and a vehicle that promotes introduction of the siNA into
5 cells of interest as described herein (e.g., using lipids and other methods of transfection known in the art, see for example Beigelman *et al.*, US 6,395,713). The kit can be used for target validation, such as in determining gene function and/or activity, or in drug optimization, and in drug discovery (see for example Usman *et al.*, USSN 60/402,996). Such a kit can also include instructions to allow a user of the kit to practice the invention.

10 The term "short interfering nucleic acid", "siNA", "short interfering RNA", "siRNA", "short interfering nucleic acid molecule", "short interfering oligonucleotide molecule", or "chemically-modified short interfering nucleic acid molecule" as used herein refers to any nucleic acid molecule capable of inhibiting or down regulating gene expression or viral replication, for example by mediating RNA interference "RNAi" or
15 gene silencing in a sequence-specific manner; see for example Zamore *et al.*, 2000, *Cell*, 101, 25-33; Bass, 2001, *Nature*, 411, 428-429; Elbashir *et al.*, 2001, *Nature*, 411, 494-498; and Kreutzer *et al.*, International PCT Publication No. WO 00/44895; Zernicka-Goetz *et al.*, International PCT Publication No. WO 01/36646; Fire, International PCT Publication No. WO 99/32619; Plaetinck *et al.*, International PCT Publication No. WO
20 00/01846; Mello and Fire, International PCT Publication No. WO 01/29058; Deschamps-Depaillette, International PCT Publication No. WO 99/07409; and Li *et al.*, International PCT Publication No. WO 00/44914; Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237; Hutvagner and Zamore, 2002,
25 *Science*, 297, 2056-60; McManus *et al.*, 2002, *RNA*, 8, 842-850; Reinhart *et al.*, 2002, *Gene & Dev.*, 16, 1616-1626; and Reinhart & Bartel, 2002, *Science*, 297, 1831). Non limiting examples of siNA molecules of the invention are shown in **Figures 4-6**, and **Tables II and III** herein. For example the siNA can be a double-stranded polynucleotide molecule comprising self-complementary sense and antisense regions,
30 wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a

portion thereof. The siNA can be assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary (i.e. each strand comprises nucleotide sequence that is complementary to nucleotide sequence in the other strand; such as where the antisense strand and sense strand form a duplex or double stranded structure, for example wherein the double stranded region is about 19 base pairs); the antisense strand comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense strand comprises nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof.

Alternatively, the siNA is assembled from a single oligonucleotide, where the self-complementary sense and antisense regions of the siNA are linked by means of a nucleic acid based or non-nucleic acid-based linker(s). The siNA can be a polynucleotide with a duplex, asymmetric duplex, hairpin or asymmetric hairpin secondary structure, having self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a separate target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siNA can be a circular single-stranded polynucleotide having two or more loop structures and a stem comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof and the sense region having nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof, and wherein the circular polynucleotide can be processed either *in vivo* or *in vitro* to generate an active siNA molecule capable of mediating RNAi. The siNA can also comprise a single stranded polynucleotide having nucleotide sequence complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof (for example, where such siNA molecule does not require the presence within the siNA molecule of nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof), wherein the single stranded polynucleotide can further comprise a terminal phosphate group, such as a 5'-phosphate (see for example Martinez *et al.*, 2002, *Cell*, 110, 563-574 and Schwarz *et al.*, 2002, *Molecular Cell*, 10, 537-568), or 5',3'-diphosphate. In certain embodiment, the siNA molecule of the invention comprises

separate sense and antisense sequences or regions, wherein the sense and antisense regions are covalently linked by nucleotide or non-nucleotide linker molecules as is known in the art, or are alternately non-covalently linked by ionic interactions, hydrogen bonding, van der Waals interactions, hydrophobic interactions, and/or stacking interactions. In certain embodiments, the siNA molecules of the invention comprise nucleotide sequence that is complementary to nucleotide sequence of a target gene. In another embodiment, the siNA molecule of the invention interacts with nucleotide sequence of a target gene in a manner that causes inhibition of expression of the target gene. As used herein, siNA molecules need not be limited to those molecules containing only RNA, but further encompasses chemically-modified nucleotides and non-nucleotides. In certain embodiments, the short interfering nucleic acid molecules of the invention lack 2'-hydroxy (2'-OH) containing nucleotides. Applicant describes in certain embodiments short interfering nucleic acids that do not require the presence of nucleotides having a 2'-hydroxy group for mediating RNAi and as such, short interfering nucleic acid molecules of the invention optionally do not include any ribonucleotides (e.g., nucleotides having a 2'-OH group). Such siNA molecules that do not require the presence of ribonucleotides within the siNA molecule to support RNAi can however have an attached linker or linkers or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. Optionally, siNA molecules can comprise ribonucleotides at about 5, 10, 20, 30, 40, or 50% of the nucleotide positions. The modified short interfering nucleic acid molecules of the invention can also be referred to as short interfering modified oligonucleotides "siMON." As used herein, the term siNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid, short interfering modified oligonucleotide, chemically-modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. In addition, as used herein, the term RNAi is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, translational inhibition, or epigenetics. For example, siNA molecules of the invention can be used to epigenetically silence genes at both the post-transcriptional level or the

pre-transcriptional level. In a non-limiting example, epigenetic regulation of gene expression by siNA molecules of the invention can result from siNA mediated modification of chromatin structure to alter gene expression (see, for example, Verdel *et al.*, 2004, *Science*, 303, 672-676; Pal-Bhadra *et al.*, 2004, *Science*, 303, 669-672; 5 Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237).

In one embodiment, a siNA molecule of the invention is a duplex forming oligonucleotide “DFO”, (see for example **Figures 14-15** and Vaish *et al.*, USSN 10 10/727,780 filed December 3, 2003).

In one embodiment, a siNA molecule of the invention is a multifunctional siNA, (see for example **Figures 16-22** and Jadhavi *et al.*, USSN (TBD) filed February 10, 2004). The multifunctional siNA of the invention can comprise sequence targeting, for example, two regions of HD RNA (see for example target sequences in **Tables II and 15 III**), such as HD sequence comprising a trinucleotide repeat region of the RNA and a SNP region of the RNA.

By “asymmetric hairpin” as used herein is meant a linear siNA molecule comprising an antisense region, a loop portion that can comprise nucleotides or non-nucleotides, and a sense region that comprises fewer nucleotides than the antisense 20 region to the extent that the sense region has enough complementary nucleotides to base pair with the antisense region and form a duplex with loop. For example, an asymmetric hairpin siNA molecule of the invention can comprise an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g. about 19 to about 22 (e.g., about 19, 20, 21, or 22) nucleotides) and a loop region comprising about 4 to about 8 25 (e.g., about 4, 5, 6, 7, or 8) nucleotides, and a sense region having about 3 to about 18 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) nucleotides that are complementary to the antisense region. The asymmetric hairpin siNA molecule can also comprise a 5'-terminal phosphate group that can be chemically modified. The loop portion of the asymmetric hairpin siNA molecule can comprise nucleotides, non- 30 nucleotides, linker molecules, or conjugate molecules as described herein.

By "asymmetric duplex" as used herein is meant a siNA molecule having two separate strands comprising a sense region and an antisense region, wherein the sense region comprises fewer nucleotides than the antisense region to the extent that the sense region has enough complementary nucleotides to base pair with the antisense region and form a duplex. For example, an asymmetric duplex siNA molecule of the invention can comprise an antisense region having length sufficient to mediate RNAi in a cell or in vitro system (e.g. about 19 to about 22 (e.g. about 19, 20, 21, or 22) nucleotides) and a sense region having about 3 to about 18 (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or 18) nucleotides that are complementary to the antisense region.

By "modulate" is meant that the expression of the gene, or level of RNA molecule or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits is up regulated or down regulated, such that expression, level, or activity is greater than or less than that observed in the absence of the modulator. For example, the term "modulate" can mean "inhibit," but the use of the word "modulate" is not limited to this definition.

By "inhibit", "down-regulate", or "reduce", it is meant that the expression of the gene, or level of RNA molecules or equivalent RNA molecules encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits, is reduced below that observed in the absence of the nucleic acid molecules (e.g., siNA) of the invention. In one embodiment, inhibition, down-regulation or reduction with an siNA molecule is below that level observed in the presence of an inactive or attenuated molecule. In another embodiment, inhibition, down-regulation, or reduction with siNA molecules is below that level observed in the presence of, for example, an siNA molecule with scrambled sequence or with mismatches. In another embodiment, inhibition, down-regulation, or reduction of gene expression with a nucleic acid molecule of the instant invention is greater in the presence of the nucleic acid molecule than in its absence.

By "gene", or "target gene", is meant, a nucleic acid that encodes an RNA, for example, nucleic acid sequences including, but not limited to, structural genes encoding a polypeptide. A gene or target gene can also encode a functional RNA (fRNA) or non-coding RNA (ncRNA), such as small temporal RNA (stRNA), micro RNA (miRNA),

small nuclear RNA (snRNA), short interfering RNA (siRNA), small nucleolar RNA (snRNA), ribosomal RNA (rRNA), transfer RNA (tRNA) and precursor RNAs thereof. Such non-coding RNAs can serve as target nucleic acid molecules for siNA mediated RNA interference in modulating the activity of fRNA or ncRNA involved in functional or regulatory cellular processes. Abberant fRNA or ncRNA activity leading to disease can therefore be modulated by siNA molecules of the invention. siNA molecules targeting fRNA and ncRNA can also be used to manipulate or alter the genotype or phenotype of an organism or cell, by intervening in cellular processes such as genetic imprinting, transcription, translation, or nucleic acid processing (e.g., transamination, methylation etc.). The target gene can be a gene derived from a cell, an endogenous gene, a transgene, or exogenous genes such as genes of a pathogen, for example a virus, which is present in the cell after infection thereof. The cell containing the target gene can be derived from or contained in any organism, for example a plant, animal, protozoan, virus, bacterium, or fungus. Non-limiting examples of plants include monocots, dicots, or gymnosperms. Non-limiting examples of animals include vertebrates or invertebrates. Non-limiting examples of fungi include molds or yeasts.

By “repeat expansion” or “RE” as used herein is meant, any protein, peptide, or polypeptide comprising a trinucleotide repeat expansion that is associated with the maintenance or development of a polyQ disease, such as Huntington disease, spinocerebellar ataxia, spinal and bulbar muscular dystrophy, and dentatorubropallidoluysian atrophy, for example as encoded by Genbank Accession Nos. shown in **Table I**. The terms “repeat expansion” or “RE” also refer to nucleic acid sequences encoding any protein, peptide, or polypeptide comprising a trinucleotide repeat expansion, such as RNA or DNA comprising trinucleotide repeat expansion encoding sequence (see for example Wood *et al.*, 2003, *Neuropathol Appl Neurobiol.*, 29, 529-45).

By “Huntingtin” or “HD” as used herein is meant, any Huntingtin protein, peptide, or polypeptide associated with the development or maintenance of Huntington disease. The terms “Huntingtin” and “HD” also refer to nucleic acid sequences encoding any huntingtin protein, peptide, or polypeptide, such as Huntingtin RNA or Huntingtin DNA (see for example Van Dellen *et al.*, January 24, 2004, *Neurogenetics*).

By “homologous sequence” is meant, a nucleotide sequence that is shared by one or more polynucleotide sequences, such as genes, gene transcripts and/or non-coding polynucleotides. For example, a homologous sequence can be a nucleotide sequence that is shared by two or more genes encoding related but different proteins, such as different members of a gene family, different protein epitopes, different protein isoforms or completely divergent genes, such as a cytokine and its corresponding receptors. A homologous sequence can be a nucleotide sequence that is shared by two or more non-coding polynucleotides, such as noncoding DNA or RNA, regulatory sequences, introns, and sites of transcriptional control or regulation. Homologous sequences can also include conserved sequence regions shared by more than one polynucleotide sequence. Homology does not need to be perfect homology (e.g., 100%), as partially homologous sequences are also contemplated by the instant invention (e.g., 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, 82%, 81%, 80% etc.).

By "conserved sequence region" is meant, a nucleotide sequence of one or more regions in a polynucleotide does not vary significantly between generations or from one biological system or organism to another biological system or organism. The polynucleotide can include both coding and non-coding DNA and RNA.

By “sense region” is meant a nucleotide sequence of a siNA molecule having complementarity to an antisense region of the siNA molecule. In addition, the sense region of a siNA molecule can comprise a nucleic acid sequence having homology with a target nucleic acid sequence.

By “antisense region” is meant a nucleotide sequence of a siNA molecule having complementarity to a target nucleic acid sequence. In addition, the antisense region of a siNA molecule can optionally comprise a nucleic acid sequence having complementarity to a sense region of the siNA molecule.

By “target nucleic acid” is meant any nucleic acid sequence whose expression or activity is to be modulated. The target nucleic acid can be DNA or RNA.

By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its complementary sequence is sufficient to
5 allow the relevant function of the nucleic acid to proceed, e.g., RNAi activity. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner *et al.*, 1987, *CSH Symp. Quant. Biol.* LII pp.123-133; Frier *et al.*, 1986, *Proc. Nat. Acad. Sci. USA* 83:9373-9377; Turner *et al.*, 1987, *J. Am. Chem. Soc.* 109:3783-3785). A percent complementarity indicates the percentage of contiguous
10 residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, or 10 nucleotides out of a total of 10 nucleotides in the first oligonucleotide being base paired to a second nucleic acid sequence having 10 nucleotides represents 50%, 60%, 70%, 80%, 90%, and 100% complementary respectively). "Perfectly complementary" means that all the
15 contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence.

The siNA molecules of the invention represent a novel therapeutic approach to treat Huntington disease and related conditions such as progressive chorea, rigidity, and dementia, and seizures, and any other diseases or conditions that are related to or will
20 respond to the levels of huntingtin in a cell or tissue, alone or in combination with other therapies. The reduction of huntingtin expression (specifically alleles associated with Huntington disease, such as polyglutamine repeat expansion and related SNPs) and thus reduction in the level of the respective protein relieves, to some extent, the symptoms of the disease or condition.

25 In one embodiment of the present invention, each sequence of a siNA molecule of the invention is independently about 18 to about 24 nucleotides in length, in specific embodiments about 18, 19, 20, 21, 22, 23, or 24 nucleotides in length. In another embodiment, the siNA duplexes of the invention independently comprise about 17 to about 23 base pairs (e.g., about 17, 18, 19, 20, 21, 22 or 23). In yet another embodiment,
30 siNA molecules of the invention comprising hairpin or circular structures are about 35 to about 55 (e.g., about 35, 40, 45, 50 or 55) nucleotides in length, or about 38 to about 44

(e.g., 38, 39, 40, 41, 42, 43 or 44) nucleotides in length and comprising about 16 to about 22 (e.g., about 16, 17, 18, 19, 20, 21 or 22) base pairs. Exemplary siNA molecules of the invention are shown in **Table II**. Exemplary synthetic siNA molecules of the invention are shown in **Table III** and/or **Figures 4-5**.

5 As used herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism, e.g., specifically does not refer to a human. The cell can be present in an organism, e.g., birds, plants and mammals such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell can be prokaryotic (e.g., bacterial cell) or eukaryotic (e.g., mammalian or plant cell). The cell can be of somatic or germ line
10 origin, totipotent or pluripotent, dividing or non-dividing. The cell can also be derived from or can comprise a gamete or embryo, a stem cell, or a fully differentiated cell.

 The siNA molecules of the invention are added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid or nucleic acid complexes can be locally administered to
15 relevant tissues *ex vivo*, or *in vivo* through injection, infusion pump or stent, with or without their incorporation in biopolymers. In particular embodiments, the nucleic acid molecules of the invention comprise sequences shown in **Tables II-III** and/or **Figures 4-5**. Examples of such nucleic acid molecules consist essentially of sequences defined in these tables and figures. Furthermore, the chemically modified constructs described in
20 **Table IV** can be applied to any siNA sequence of the invention.

 In another aspect, the invention provides mammalian cells containing one or more siNA molecules of this invention. The one or more siNA molecules can independently be targeted to the same or different sites.

 By "RNA" is meant a molecule comprising at least one ribonucleotide residue. By
25 "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2' position of a β -D-ribo-furanose moiety. The terms include double-stranded RNA, single-stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more
30 nucleotides. Such alterations can include addition of non-nucleotide material, such as to

the end(s) of the siNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in the RNA molecules of the instant invention can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as
5 analogs or analogs of naturally-occurring RNA.

By "subject" is meant an organism, which is a donor or recipient of explanted cells or the cells themselves. "Subject" also refers to an organism to which the nucleic acid molecules of the invention can be administered. A subject can be a mammal or mammalian cells, including a human or human cells.

10 The term "phosphorothioate" as used herein refers to an internucleotide linkage having Formula I, wherein Z and/or W comprise a sulfur atom. Hence, the term phosphorothioate refers to both phosphorothioate and phosphorodithioate internucleotide linkages.

The term "phosphonoacetate" as used herein refers to an internucleotide linkage
15 having Formula I, wherein Z and/or W comprise an acetyl or protected acetyl group.

The term "thiophosphonoacetate" as used herein refers to an internucleotide linkage having Formula I, wherein Z comprises an acetyl or protected acetyl group and W comprises a sulfur atom or alternately W comprises an acetyl or protected acetyl group and Z comprises a sulfur atom.

20 The term "universal base" as used herein refers to nucleotide base analogs that form base pairs with each of the natural DNA/RNA bases with little discrimination between them. Non-limiting examples of universal bases include C-phenyl, C-naphthyl and other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-nitroindole as known in the art
25 (see for example Loakes, 2001, *Nucleic Acids Research*, 29, 2437-2447).

The term "acyclic nucleotide" as used herein refers to any nucleotide having an acyclic ribose sugar, for example where any of the ribose carbons (C1, C2, C3, C4, or C5), are independently or in combination absent from the nucleotide.

The nucleic acid molecules of the instant invention, individually, or in combination or in conjunction with other drugs, can be used to treat diseases or conditions discussed herein (e.g., cancers and othe proliferative conditions). For example, to treat a particular disease or condition, the siNA molecules can be administered to a subject or can be
5 administered to other appropriate cells evident to those skilled in the art, individually or in combination with one or more drugs under conditions suitable for the treatment.

In a further embodiment, the siNA molecules can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the described molecules could be used in combination with one or more known therapeutic
10 agents to treat a disease or condition. Non-limiting examples of other therapeutic agents that can be readily combined with a siNA molecule of the invention are enzymatic nucleic acid molecules, allosteric nucleic acid molecules, antisense, decoy, or aptamer nucleic acid molecules, antibodies such as monoclonal antibodies, small molecules, and other organic and/or inorganic compounds including metals, salts and ions.

15 In one embodiment, the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the invention, in a manner which allows expression of the siNA molecule. For example, the vector can contain sequence(s) encoding both strands of a siNA molecule comprising a duplex. The vector can also contain sequence(s) encoding a single nucleic acid molecule that is self-
20 complementary and thus forms a siNA molecule. Non-limiting examples of such expression vectors are described in Paul *et al.*, 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725.

25 In another embodiment, the invention features a mammalian cell, for example, a human cell, including an expression vector of the invention.

In yet another embodiment, the expression vector of the invention comprises a sequence for a siNA molecule having complementarity to a RNA molecule referred to by a Genbank Accession numbers, for example Genbank Accession Nos. shown in **Table I**.

In one embodiment, an expression vector of the invention comprises a nucleic acid sequence encoding two or more siNA molecules, which can be the same or different.

In another aspect of the invention, siNA molecules that interact with target RNA molecules and down-regulate gene encoding target RNA molecules (for example target RNA molecules referred to by Genbank Accession numbers herein) are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecules bind and down-regulate gene function or expression via RNA interference (RNAi). Delivery of siNA expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into the subject, or by any other means that would allow for introduction into the desired target cell.

By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a non-limiting example of a scheme for the synthesis of siNA molecules. The complementary siNA sequence strands, strand 1 and strand 2, are synthesized in tandem and are connected by a cleavable linkage, such as a nucleotide succinate or abasic succinate, which can be the same or different from the cleavable linker used for solid phase synthesis on a solid support. The synthesis can be either solid phase or solution phase, in the example shown, the synthesis is a solid phase synthesis. The synthesis is performed such that a protecting group, such as a dimethoxytrityl group,

remains intact on the terminal nucleotide of the tandem oligonucleotide. Upon cleavage and deprotection of the oligonucleotide, the two siNA strands spontaneously hybridize to form a siNA duplex, which allows the purification of the duplex by utilizing the properties of the terminal protecting group, for example by applying a trityl on
 5 purification method wherein only duplexes/oligonucleotides with the terminal protecting group are isolated.

Figure 2 shows a MALDI-TOF mass spectrum of a purified siNA duplex synthesized by a method of the invention. The two peaks shown correspond to the predicted mass of the separate siNA sequence strands. This result demonstrates that the
 10 siNA duplex generated from tandem synthesis can be purified as a single entity using a simple trityl-on purification methodology.

Figure 3 shows a non-limiting proposed mechanistic representation of target RNA degradation involved in RNAi. Double-stranded RNA (dsRNA), which is generated by RNA-dependent RNA polymerase (RdRP) from foreign single-stranded RNA, for
 15 example viral, transposon, or other exogenous RNA, activates the DICER enzyme that in turn generates siNA duplexes. Alternately, synthetic or expressed siNA can be introduced directly into a cell by appropriate means. An active siNA complex forms which recognizes a target RNA, resulting in degradation of the target RNA by the RISC endonuclease complex or in the synthesis of additional RNA by RNA-dependent RNA
 20 polymerase (RdRP), which can activate DICER and result in additional siNA molecules, thereby amplifying the RNAi response.

Figure 4A-F shows non-limiting examples of chemically-modified siNA constructs of the present invention. In the figure, N stands for any nucleotide (adenosine, guanosine, cytosine, uridine, or optionally thymidine, for example thymidine can be
 25 substituted in the overhanging regions designated by parenthesis (N N). Various modifications are shown for the sense and antisense strands of the siNA constructs.

Figure 4A: The sense strand comprises 21 nucleotides wherein the two terminal 3'-nucleotides are optionally base paired and wherein all nucleotides present are ribonucleotides except for (N N) nucleotides, which can comprise ribonucleotides,
 30 deoxynucleotides, universal bases, or other chemical modifications described herein.

The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all nucleotides present are ribonucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s", optionally connects the (N N) nucleotides in the antisense strand.

Figure 4B: The sense strand comprises 21 nucleotides wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as "s", optionally connects the (N N) nucleotides in the sense and antisense strand.

Figure 4C: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-O-methyl or 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that

may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s”, optionally connects the (N N) nucleotides in the antisense strand.

Figure 4D: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and wherein all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s”, optionally connects the (N N) nucleotides in the antisense strand.

Figure 4E: The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides and all purine nucleotides that may be present are 2'-O-methyl modified nucleotides except for (N N) nucleotides, which can comprise

ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s”, optionally connects the (N N) nucleotides in the antisense strand.

5 **Figure 4F:** The sense strand comprises 21 nucleotides having 5'- and 3'- terminal cap moieties wherein the two terminal 3'-nucleotides are optionally base paired and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro modified nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein and
10 wherein and all purine nucleotides that may be present are 2'-deoxy nucleotides. The antisense strand comprises 21 nucleotides, optionally having a 3'-terminal glyceryl moiety and wherein the two terminal 3'-nucleotides are optionally complementary to the target RNA sequence, and having one 3'-terminal phosphorothioate internucleotide linkage and wherein all pyrimidine nucleotides that may be present are 2'-deoxy-2'-fluoro
15 modified nucleotides and all purine nucleotides that may be present are 2'-deoxy nucleotides except for (N N) nucleotides, which can comprise ribonucleotides, deoxynucleotides, universal bases, or other chemical modifications described herein. A modified internucleotide linkage, such as a phosphorothioate, phosphorodithioate or other modified internucleotide linkage as described herein, shown as “s”, optionally
20 connects the (N N) nucleotides in the antisense strand. The antisense strand of constructs A-F comprise sequence complementary to any target nucleic acid sequence of the invention. Furthermore, when a glyceryl moiety (L) is present at the 3'-end of the antisense strand for any construct shown in Figure 4 A-F, the modified internucleotide linkage is optional.

25 **Figure 5A-F** shows non-limiting examples of specific chemically-modified siNA sequences of the invention. A-F applies the chemical modifications described in **Figure 4A-F** to a HD siNA sequence. Such chemical modifications can be applied to any repeat expansion sequence and/or related SNP sequence.

30 **Figure 6** shows non-limiting examples of different siNA constructs of the invention. The examples shown (constructs 1, 2, and 3) have 19 representative base pairs; however, different embodiments of the invention include any number of base pairs

described herein. Bracketed regions represent nucleotide overhangs, for example comprising about 1, 2, 3, or 4 nucleotides in length, preferably about 2 nucleotides. Constructs 1 and 2 can be used independently for RNAi activity. Construct 2 can comprise a polynucleotide or non-nucleotide linker, which can optionally be designed as a biodegradable linker. In one embodiment, the loop structure shown in construct 2 can comprise a biodegradable linker that results in the formation of construct 1 *in vivo* and/or *in vitro*. In another example, construct 3 can be used to generate construct 2 under the same principle wherein a linker is used to generate the active siNA construct 2 *in vivo* and/or *in vitro*, which can optionally utilize another biodegradable linker to generate the active siNA construct 1 *in vivo* and/or *in vitro*. As such, the stability and/or activity of the siNA constructs can be modulated based on the design of the siNA construct for use *in vivo* or *in vitro* and/or *in vitro*.

Figure 7A-C is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate siNA hairpin constructs.

Figure 7A: A DNA oligomer is synthesized with a 5'-restriction site (R1) sequence followed by a region having sequence identical (sense region of siNA) to a predetermined HD target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, which is followed by a loop sequence of defined sequence (X), comprising, for example, about 3 to about 10 nucleotides.

Figure 7B: The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence that will result in a siNA transcript having specificity for a HD target sequence and having self-complementary sense and antisense regions.

Figure 7C: The construct is heated (for example to about 95°C) to linearize the sequence, thus allowing extension of a complementary second DNA strand using a primer to the 3'-restriction sequence of the first strand. The double-stranded DNA is then inserted into an appropriate vector for expression in cells. The construct can be designed such that a 3'-terminal nucleotide overhang results from the transcription, for example by engineering restriction sites and/or utilizing a poly-U termination region as described in Paul *et al.*, 2002, *Nature Biotechnology*, 29, 505-508.

Figure 8A-C is a diagrammatic representation of a scheme utilized in generating an expression cassette to generate double-stranded siNA constructs.

Figure 8A: A DNA oligomer is synthesized with a 5'-restriction (R1) site sequence followed by a region having sequence identical (sense region of siNA) to a predetermined HD target sequence, wherein the sense region comprises, for example, about 19, 20, 21, or 22 nucleotides (N) in length, and which is followed by a 3'-restriction site (R2) which is adjacent to a loop sequence of defined sequence (X).

Figure 8B: The synthetic construct is then extended by DNA polymerase to generate a hairpin structure having self-complementary sequence.

Figure 8C: The construct is processed by restriction enzymes specific to R1 and R2 to generate a double-stranded DNA which is then inserted into an appropriate vector for expression in cells. The transcription cassette is designed such that a U6 promoter region flanks each side of the dsDNA which generates the separate sense and antisense strands of the siNA. Poly T termination sequences can be added to the constructs to generate U overhangs in the resulting transcript.

Figure 9A-E is a diagrammatic representation of a method used to determine target sites for siNA mediated RNAi within a particular target nucleic acid sequence, such as messenger RNA.

Figure 9A: A pool of siNA oligonucleotides are synthesized wherein the antisense region of the siNA constructs has complementarity to target sites across the target nucleic acid sequence, and wherein the sense region comprises sequence complementary to the antisense region of the siNA.

Figure 9B&C: (**Figure 9B**) The sequences are pooled and are inserted into vectors such that (**Figure 9C**) transfection of a vector into cells results in the expression of the siNA.

Figure 9D: Cells are sorted based on phenotypic change that is associated with modulation of the target nucleic acid sequence.

Figure 9E: The siNA is isolated from the sorted cells and is sequenced to identify efficacious target sites within the target nucleic acid sequence.

Figure 10 shows non-limiting examples of different stabilization chemistries (1-10) that can be used, for example, to stabilize the 3'-end of siNA sequences of the invention, including (1) [3-3']-inverted deoxyribose; (2) deoxyribonucleotide; (3) [5'-3']-3'-deoxyribonucleotide; (4) [5'-3']-ribonucleotide; (5) [5'-3']-3'-O-methyl ribonucleotide; (6) 3'-glyceryl; (7) [3'-5']-3'-deoxyribonucleotide; (8) [3'-3']-deoxyribonucleotide; (9) [5'-2']-deoxyribonucleotide; and (10) [5-3']-dideoxyribonucleotide. In addition to modified and unmodified backbone chemistries indicated in the figure, these chemistries can be combined with different backbone modifications as described herein, for example, backbone modifications having Formula I. In addition, the 2'-deoxy nucleotide shown 5' to the terminal modifications shown can be another modified or unmodified nucleotide or non-nucleotide described herein, for example modifications having any of Formulae I-VII or any combination thereof.

Figure 11 shows a non-limiting example of a strategy used to identify chemically modified siNA constructs of the invention that are nuclease resistance while preserving the ability to mediate RNAi activity. Chemical modifications are introduced into the siNA construct based on educated design parameters (e.g. introducing 2'-modifications, base modifications, backbone modifications, terminal cap modifications etc). The modified construct is tested in an appropriate system (e.g. human serum for nuclease resistance, shown, or an animal model for PK/delivery parameters). In parallel, the siNA construct is tested for RNAi activity, for example in a cell culture system such as a luciferase reporter assay). Lead siNA constructs are then identified which possess a particular characteristic while maintaining RNAi activity, and can be further modified and assayed once again. This same approach can be used to identify siNA-conjugate molecules with improved pharmacokinetic profiles, delivery, and RNAi activity.

Figure 12 shows non-limiting examples of phosphorylated siNA molecules of the invention, including linear and duplex constructs and asymmetric derivatives thereof.

Figure 13 shows non-limiting examples of chemically modified terminal phosphate groups of the invention.

Figure 14A shows a non-limiting example of methodology used to design self complementary DFO constructs utilizing palidrome and/or repeat nucleic acid sequences that are identified in a target nucleic acid sequence. (i) A palindrome or repeat sequence is identified in a nucleic acid target sequence. (ii) A sequence is designed that is complementary to the target nucleic acid sequence and the palindrome sequence. (iii) An inverse repeat sequence of the non-palindrome/repeat portion of the complementary sequence is appended to the 3'-end of the complementary sequence to generate a self complmentary DFO molecule comprising sequence complementary to the nucleic acid target. (iv) The DFO molecule can self-assemble to form a double stranded oligonucleotide. **Figure 14B** shows a non-limiting representative example of a duplex forming oligonucleotide sequence. **Figure 14C** shows a non-limiting example of the self assembly schematic of a representative duplex forming oligonucleotide sequence. **Figure 14D** shows a non-limiting example of the self assembly schematic of a representative duplex forming oligonucleotide sequence followed by interaction with a target nucleic acid sequence resulting in modulation of gene expression.

Figure 15 shows a non-limiting example of the design of self complementary DFO constructs utilizing palidrome and/or repeat nucleic acid sequences that are incorporated into the DFO constructs that have sequence complementary to any target nucleic acid sequence of interest. Incorporation of these palindrome/repeat sequences allow the design of DFO constructs that form duplexes in which each strand is capable of mediating modulation of target gene expression, for example by RNAi. First, the target sequence is identified. A complementary sequence is then generated in which nucleotide or non-nucleotide modifications (shown as X or Y) are introduced into the complementary sequence that generate an artificial palindrome (shown as XYXYXY in the Figure). An inverse repeat of the non-palindrome/repeat complementary sequence is appended to the 3'-end of the complementary sequence to generate a self complimentary DFO comprising sequence complementary to the nucleic acid target. The DFO can self-assemble to form a double stranded oligonucleotide.

Figure 16 shows non-limiting examples of multifunctional siNA molecules of the invention comprising two separate polynucleotide sequences that are each capable of mediating RNAi directed cleavage of differing target nucleic acid sequences. **Figure**

16A shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first and second complementary regions are situated at the 3'-ends of each polynucleotide sequence in the multifunctional siNA. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. **Figure 16B** shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first and second complementary regions are situated at the 5'-ends of each polynucleotide sequence in the multifunctional siNA. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences.

Figure 17 shows non-limiting examples of multifunctional siNA molecules of the invention comprising a single polynucleotide sequence comprising distinct regions that are each capable of mediating RNAi directed cleavage of differing target nucleic acid sequences. **Figure 17A** shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the second complementary region is situated at the 3'-end of the polynucleotide sequence in the multifunctional siNA. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. **Figure 17B** shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first complementary region is situated at the 5'-end of the polynucleotide sequence in the

multifunctional siNA. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. In one embodiment, these multifunctional siNA constructs are processed in vivo or in vitro to generate multifunctional siNA constructs as shown in **Figure 16**.

Figure 18 shows non-limiting examples of multifunctional siNA molecules of the invention comprising two separate polynucleotide sequences that are each capable of mediating RNAi directed cleavage of differing target nucleic acid sequences and wherein the multifunctional siNA construct further comprises a self complementary, palindrome, or repeat region, thus enabling shorter bifunctional siNA constructs that can mediate RNA interference against differing target nucleic acid sequences. **Figure 18A** shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first and second complementary regions are situated at the 3'-ends of each polynucleotide sequence in the multifunctional siNA, and wherein the first and second complementary regions further comprise a self complementary, palindrome, or repeat region. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. **Figure 18B** shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first and second complementary regions are situated at the 5'-ends of each polynucleotide sequence in the multifunctional siNA, and wherein the first and second complementary regions further comprise a self complementary, palindrome, or repeat region. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences.

Figure 19 shows non-limiting examples of multifunctional siNA molecules of the invention comprising a single polynucleotide sequence comprising distinct regions that are each capable of mediating RNAi directed cleavage of differing target nucleic acid sequences and wherein the multifunctional siNA construct further comprises a self complementary, palindrome, or repeat region, thus enabling shorter bifunctional siNA constructs that can mediate RNA interference against differing target nucleic acid sequences. **Figure 19A** shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the second complementary region is situated at the 3'-end of the polynucleotide sequence in the multifunctional siNA, and wherein the first and second complementary regions further comprise a self complementary, palindrome, or repeat region. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. **Figure 19B** shows a non-limiting example of a multifunctional siNA molecule having a first region that is complementary to a first target nucleic acid sequence (complementary region 1) and a second region that is complementary to a second target nucleic acid sequence (complementary region 2), wherein the first complementary region is situated at the 5'-end of the polynucleotide sequence in the multifunctional siNA, and wherein the first and second complementary regions further comprise a self complementary, palindrome, or repeat region. The dashed portions of each polynucleotide sequence of the multifunctional siNA construct have complementarity with regard to corresponding portions of the siNA duplex, but do not have complementarity to the target nucleic acid sequences. In one embodiment, these multifunctional siNA constructs are processed in vivo or in vitro to generate multifunctional siNA constructs as shown in **Figure 18**.

Figure 20 shows a non-limiting example of how multifunctional siNA molecules of the invention can target two separate target nucleic acid molecules, such as separate RNA molecules encoding differing proteins, for example a cytokine and its corresponding receptor, differing viral strains, a virus and a cellular protein involved in viral infection or replication, or differing proteins involved in a common or divergent

biologic pathway that is implicated in the maintenance of progression of disease. Each strand of the multifunctional siNA construct comprises a region having complementarity to separate target nucleic acid molecules. The multifunctional siNA molecule is designed such that each strand of the siNA can be utilized by the RISC complex to initiate RNA interference mediated cleavage of its corresponding target. These design parameters can include destabilization of each end of the siNA construct (see for example Schwarz *et al.*, 2003, *Cell*, 115, 199-208). Such destabilization can be accomplished for example by using guanosine-cytidine base pairs, alternate base pairs (e.g., wobbles), or destabilizing chemically modified nucleotides at terminal nucleotide positions as is known in the art.

Figure 21 shows a non-limiting example of how multifunctional siNA molecules of the invention can target two separate target nucleic acid sequences within the same target nucleic acid molecule, such as alternate coding regions of a RNA, coding and non-coding regions of a RNA, or alternate splice variant regions of a RNA. Each strand of the multifunctional siNA construct comprises a region having complementarity to the separate regions of the target nucleic acid molecule. The multifunctional siNA molecule is designed such that each strand of the siNA can be utilized by the RISC complex to initiate RNA interference mediated cleavage of its corresponding target region. These design parameters can include destabilization of each end of the siNA construct (see for example Schwarz *et al.*, 2003, *Cell*, 115, 199-208). Such destabilization can be accomplished for example by using guanosine-cytidine base pairs, alternate base pairs (e.g., wobbles), or destabilizing chemically modified nucleotides at terminal nucleotide positions as is known in the art.

Figure 22 shows a non-limiting example of siNA mediated inhibition of expression of myc-tagged human HD protein in HEK-293 cells transfected with active and inverted control siNA constructs along with untreated and transfection controls.

DETAILED DESCRIPTION OF THE INVENTION

Mechanism of action of Nucleic Acid Molecules of the Invention

The discussion that follows discusses the proposed mechanism of RNA interference mediated by short interfering RNA as is presently known, and is not meant to be limiting and is not an admission of prior art. Applicant demonstrates herein that chemically-modified short interfering nucleic acids possess similar or improved capacity to mediate RNAi as do siRNA molecules and are expected to possess improved stability and activity *in vivo*; therefore, this discussion is not meant to be limiting only to siRNA and can be applied to siNA as a whole. By "improved capacity to mediate RNAi" or "improved RNAi activity" is meant to include RNAi activity measured *in vitro* and/or *in vivo* where the RNAi activity is a reflection of both the ability of the siNA to mediate RNAi and the stability of the siNAs of the invention. In this invention, the product of these activities can be increased *in vitro* and/or *in vivo* compared to an all RNA siRNA or a siNA containing a plurality of ribonucleotides. In some cases, the activity or stability of the siNA molecule can be decreased (i.e., less than ten-fold), but the overall activity of the siNA molecule is enhanced *in vitro* and/or *in vivo*.

RNA interference refers to the process of sequence specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire *et al.*, 1998, *Nature*, 391, 806). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes which is commonly shared by diverse flora and phyla (Fire *et al.*, 1999, *Trends Genet.*, 15, 358). Such protection from foreign gene expression may have evolved in response to the production of double-stranded RNAs (dsRNAs) derived from viral infection or the random integration of transposon elements into a host genome via a cellular response that specifically destroys homologous single-stranded RNA or viral genomic RNA. The presence of dsRNA in cells triggers the RNAi response through a mechanism that has yet to be fully characterized. This mechanism appears to be different from the interferon response that results from dsRNA-mediated activation of protein kinase PKR and 2', 5'-oligoadenylate synthetase resulting in non-specific cleavage of mRNA by ribonuclease L.

The presence of long dsRNAs in cells stimulates the activity of a ribonuclease III enzyme referred to as Dicer. Dicer is involved in the processing of the dsRNA into short pieces of dsRNA known as short interfering RNAs (siRNAs) (Bernstein *et al.*, 2001, *Nature*, 409, 363). Short interfering RNAs derived from Dicer activity are typically
5 about 21 to about 23 nucleotides in length and comprise about 19 base pair duplexes. Dicer has also been implicated in the excision of 21- and 22-nucleotide small temporal RNAs (stRNAs) from precursor RNA of conserved structure that are implicated in translational control (Hutvagner *et al.*, 2001, *Science*, 293, 834). The RNAi response also features an endonuclease complex containing a siRNA, commonly referred to as an
10 RNA-induced silencing complex (RISC), which mediates cleavage of single-stranded RNA having sequence homologous to the siRNA. Cleavage of the target RNA takes place in the middle of the region complementary to the guide sequence of the siRNA duplex (Elbashir *et al.*, 2001, *Genes Dev.*, 15, 188). In addition, RNA interference can also involve small RNA (e.g., micro-RNA or miRNA) mediated gene silencing,
15 presumably through cellular mechanisms that regulate chromatin structure and thereby prevent transcription of target gene sequences (see for example Allshire, 2002, *Science*, 297, 1818-1819; Volpe *et al.*, 2002, *Science*, 297, 1833-1837; Jenuwein, 2002, *Science*, 297, 2215-2218; and Hall *et al.*, 2002, *Science*, 297, 2232-2237). As such, siRNA molecules of the invention can be used to mediate gene silencing via interaction with
20 RNA transcripts or alternately by interaction with particular gene sequences, wherein such interaction results in gene silencing either at the transcriptional level or post-transcriptional level.

RNAi has been studied in a variety of systems. Fire *et al.*, 1998, *Nature*, 391, 806, were the first to observe RNAi in *C. elegans*. Wianny and Goetz, 1999, *Nature Cell Biol.*, 2, 70, describe RNAi mediated by dsRNA in mouse embryos. Hammond *et al.*,
25 2000, *Nature*, 404, 293, describe RNAi in *Drosophila* cells transfected with dsRNA. Elbashir *et al.*, 2001, *Nature*, 411, 494, describe RNAi induced by introduction of duplexes of synthetic 21-nucleotide RNAs in cultured mammalian cells including human embryonic kidney and HeLa cells. Recent work in *Drosophila* embryonic lysates has
30 revealed certain requirements for siRNA length, structure, chemical composition, and sequence that are essential to mediate efficient RNAi activity. These studies have shown that 21 nucleotide siRNA duplexes are most active when containing two 2-nucleotide 3'-

terminal nucleotide overhangs. Furthermore, substitution of one or both siRNA strands with 2'-deoxy or 2'-O-methyl nucleotides abolishes RNAi activity, whereas substitution of 3'-terminal siRNA nucleotides with deoxy nucleotides was shown to be tolerated. Mismatch sequences in the center of the siRNA duplex were also shown to abolish RNAi activity. In addition, these studies also indicate that the position of the cleavage site in the target RNA is defined by the 5'-end of the siRNA guide sequence rather than the 3'-end (Elbashir *et al.*, 2001, *EMBO J.*, 20, 6877). Other studies have indicated that a 5'-phosphate on the target-complementary strand of a siRNA duplex is required for siRNA activity and that ATP is utilized to maintain the 5'-phosphate moiety on the siRNA (Nykanen *et al.*, 2001, *Cell*, 107, 309); however, siRNA molecules lacking a 5'-phosphate are active when introduced exogenously, suggesting that 5'-phosphorylation of siRNA constructs may occur *in vivo*.

Synthesis of Nucleic acid Molecules

Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small" refers to nucleic acid motifs no more than 100 nucleotides in length, preferably no more than 80 nucleotides in length, and most preferably no more than 50 nucleotides in length; *e.g.*, individual siNA oligonucleotide sequences or siNA sequences synthesized in tandem) are preferably used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of protein and/or RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

Oligonucleotides (*e.g.*, certain modified oligonucleotides or portions of oligonucleotides lacking ribonucleotides) are synthesized using protocols known in the art, for example as described in Caruthers *et al.*, 1992, *Methods in Enzymology* 211, 3-19, Thompson *et al.*, International PCT Publication No. WO 99/54459, Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684, Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, Brennan *et al.*, 1998, *Biotechnol Bioeng.*, 61, 33-45, and Brennan, U.S. Pat. No. 6,001,311. All of these references are incorporated herein by reference. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-

limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μmol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 second coupling step for 2'-deoxy nucleotides or 2'-deoxy-2'-fluoro nucleotides. **Table V** outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μmol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 μL of 0.11 M = 6.6 μmol) of 2'-O-methyl phosphoramidite and a 105-fold excess of S-ethyl tetrazole (60 μL of 0.25 M = 15 μmol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 22-fold excess (40 μL of 0.11 M = 4.4 μmol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40 μL of 0.25 M = 10 μmol) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution is 16.9 mM I_2 , 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide, 0.05 M in acetonitrile) is used.

Deprotection of the DNA-based oligonucleotides is performed as follows: the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aqueous methylamine (1 mL) at 65 °C for 10 minutes. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder.

The method of synthesis used for RNA including certain siNA molecules of the invention follows the procedure as described in Usman *et al.*, 1987, *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.*, 1990, *Nucleic Acids Res.*, 18, 5433; and Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677-2684 Wincott *et al.*, 1997, *Methods Mol. Bio.*, 74, 59, and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 μmol scale protocol with a 7.5 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides.

Table V outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 μmol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 μL of 0.11 M = 6.6 μmol) of 2'-O-methyl phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60 μL of 0.25 M = 15 μmol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 66-fold excess (120 μL of 0.11 M = 13.2 μmol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120 μL of 0.25 M = 30 μmol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include the following: detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% *N*-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I_2 , 49 mM pyridine, 9% water in THF (PERSEPTIVE™). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide 0.05 M in acetonitrile) is used.

Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1

mL) at 65 °C for 10 min. After cooling to –20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H₂O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300 µL of a solution of 1.5 mL N-methylpyrrolidinone, 750 µL TEA and 1 mL TEA•3HF to provide a 1.4 M HF concentration) and heated to 65 °C. After 1.5 h, the oligomer is quenched with 1.5 M NH₄HCO₃.

Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 33% ethanolic methylamine/DMSO: 1/1 (0.8 mL) at 65 °C for 15 minutes. The vial is brought to room temperature TEA•3HF (0.1 mL) is added and the vial is heated at 65 °C for 15 minutes. The sample is cooled at –20 °C and then quenched with 1.5 M NH₄HCO₃.

For purification of the trityl-on oligomers, the quenched NH₄HCO₃ solution is loaded onto a C-18 containing cartridge that had been prewashed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA is detritylated with 0.5% TFA for 13 minutes. The cartridge is then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide is then eluted with 30% acetonitrile.

The average stepwise coupling yields are typically >98% (Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684). Those of ordinary skill in the art will recognize that the scale of synthesis can be adapted to be larger or smaller than the example described above including but not limited to 96-well format.

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example, by ligation (Moore *et al.*, 1992, *Science* 256, 9923; Draper *et al.*, International PCT publication No. WO 93/23569; Shabarova *et al.*, 1991, *Nucleic Acids Research* 19, 4247; Bellon *et al.*, 1997, *Nucleosides & Nucleotides*, 16, 951; Bellon *et al.*, 1997, *Bioconjugate Chem.* 8, 204), or by hybridization following synthesis and/or deprotection.

The siNA molecules of the invention can also be synthesized via a tandem synthesis methodology as described in Example 1 herein, wherein both siNA strands are synthesized as a single contiguous oligonucleotide fragment or strand separated by a cleavable linker which is subsequently cleaved to provide separate siNA fragments or strands that hybridize and permit purification of the siNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker. The tandem synthesis of siNA as described herein can be readily adapted to both multiwell/multiplate synthesis platforms such as 96 well or similarly larger multi-well platforms. The tandem synthesis of siNA as described herein can also be readily adapted to large scale synthesis platforms employing batch reactors, synthesis columns and the like.

A siNA molecule can also be assembled from two distinct nucleic acid strands or fragments wherein one fragment includes the sense region and the second fragment includes the antisense region of the RNA molecule.

The nucleic acid molecules of the present invention can be modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992, *TIBS* 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163). siNA constructs can be purified by gel electrophoresis using general methods or can be purified by high pressure liquid chromatography (HPLC; see Wincott *et al.*, *supra*, the totality of which is hereby incorporated herein by reference) and re-suspended in water.

In another aspect of the invention, siNA molecules of the invention are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the siNA molecules can be delivered as described herein, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of siNA molecules.

Optimizing Activity of the nucleic acid molecule of the invention.

Chemically synthesizing nucleic acid molecules with modifications (base, sugar and/or phosphate) can prevent their degradation by serum ribonucleases, which can

increase their potency (see *e.g.*, Eckstein *et al.*, International Publication No. WO 92/07065; Perrault *et al.*, 1990 *Nature* 344, 565; Pieken *et al.*, 1991, *Science* 253, 314; Usman and Cedergren, 1992, *Trends in Biochem. Sci.* 17, 334; Usman *et al.*, International Publication No. WO 93/15187; and Rossi *et al.*, International Publication No. WO 91/03162; Sproat, U.S. Pat. No. 5,334,711; Gold *et al.*, U.S. Pat. No. 6,300,074; and Burgin *et al.*, *supra*; all of which are incorporated by reference herein). All of the above references describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of the nucleic acid molecules described herein. Modifications that enhance their efficacy in cells, and removal of bases from nucleic acid molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired.

There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules with significant enhancement in their nuclease stability and efficacy. For example, oligonucleotides are modified to enhance stability and/or enhance biological activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-fluoro, 2'-O-methyl, 2'-O-allyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992, *TIBS* 17, 34; Usman *et al.*, 1994, *Nucleic Acids Symp. Ser.* 31, 163; Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). Sugar modification of nucleic acid molecules have been extensively described in the art (see Eckstein *et al.*, International Publication PCT No. WO 92/07065; Perrault *et al.* *Nature*, 1990, 344, 565-568; Pieken *et al.* *Science*, 1991, 253, 314-317; Usman and Cedergren, *Trends in Biochem. Sci.*, 1992, 17, 334-339; Usman *et al.* International Publication PCT No. WO 93/15187; Sproat, U.S. Pat. No. 5,334,711 and Beigelman *et al.*, 1995, *J. Biol. Chem.*, 270, 25702; Beigelman *et al.*, International PCT publication No. WO 97/26270; Beigelman *et al.*, U.S. Pat. No. 5,716,824; Usman *et al.*, U.S. Pat. No. 5,627,053; Woolf *et al.*, International PCT Publication No. WO 98/13526; Thompson *et al.*, USSN 60/082,404 which was filed on April 20, 1998; Karpeisky *et al.*, 1998, *Tetrahedron Lett.*, 39, 1131; Earnshaw and Gait, 1998, *Biopolymers (Nucleic Acid Sciences)*, 48, 39-55; Verma and Eckstein, 1998, *Annu. Rev. Biochem.*, 67, 99-134; and Burlina *et al.*, 1997, *Bioorg. Med. Chem.*, 5, 1999-2010; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of

incorporation of sugar, base and/or phosphate modifications and the like into nucleic acid molecules without modulating catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify the siNA nucleic acid molecules of the instant invention so long as the ability of siNA to promote RNAi in cells is not significantly inhibited.

While chemical modification of oligonucleotide internucleotide linkages with phosphorothioate, phosphorodithioate, and/or 5'-methylphosphonate linkages improves stability, excessive modifications can cause some toxicity or decreased activity. Therefore, when designing nucleic acid molecules, the amount of these internucleotide linkages should be minimized. The reduction in the concentration of these linkages should lower toxicity, resulting in increased efficacy and higher specificity of these molecules.

Short interfering nucleic acid (siNA) molecules having chemical modifications that maintain or enhance activity are provided. Such a nucleic acid is also generally more resistant to nucleases than an unmodified nucleic acid. Accordingly, the *in vitro* and/or *in vivo* activity should not be significantly lowered. In cases in which modulation is the goal, therapeutic nucleic acid molecules delivered exogenously should optimally be stable within cells until translation of the target RNA has been modulated long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Improvements in the chemical synthesis of RNA and DNA (Wincott *et al.*, 1995, *Nucleic Acids Res.* 23, 2677; Caruthers *et al.*, 1992, *Methods in Enzymology* 211,3-19 (incorporated by reference herein)) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability, as described above.

In one embodiment, nucleic acid molecules of the invention include one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) G-clamp nucleotides. A G-clamp nucleotide is a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine within a duplex, see for example Lin and Matteucci, 1998, *J. Am. Chem. Soc.*, 120, 8531-8532. A single G-clamp analog substitution within an oligonucleotide can result in substantially enhanced helical thermal stability and mismatch discrimination when

hybridized to complementary oligonucleotides. The inclusion of such nucleotides in nucleic acid molecules of the invention results in both enhanced affinity and specificity to nucleic acid targets, complementary sequences, or template strands. In another embodiment, nucleic acid molecules of the invention include one or more (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more) LNA "locked nucleic acid" nucleotides such as a 2', 4'-C methylene bicyclo nucleotide (see for example Wengel *et al.*, International PCT Publication No. WO 00/66604 and WO 99/14226).

In another embodiment, the invention features conjugates and/or complexes of siNA molecules of the invention. Such conjugates and/or complexes can be used to facilitate delivery of siNA molecules into a biological system, such as a cell. The conjugates and complexes provided by the instant invention can impart therapeutic activity by transferring therapeutic compounds across cellular membranes, altering the pharmacokinetics, and/or modulating the localization of nucleic acid molecules of the invention. The present invention encompasses the design and synthesis of novel conjugates and complexes for the delivery of molecules, including, but not limited to, small molecules, lipids, cholesterol, phospholipids, nucleosides, nucleotides, nucleic acids, antibodies, toxins, negatively charged polymers and other polymers, for example proteins, peptides, hormones, carbohydrates, polyethylene glycols, or polyamines, across cellular membranes. In general, the transporters described are designed to be used either individually or as part of a multi-component system, with or without degradable linkers. These compounds are expected to improve delivery and/or localization of nucleic acid molecules of the invention into a number of cell types originating from different tissues, in the presence or absence of serum (see Sullenger and Cech, U.S. Pat. No. 5,854,038). Conjugates of the molecules described herein can be attached to biologically active molecules via linkers that are biodegradable, such as biodegradable nucleic acid linker molecules.

The term "biodegradable linker" as used herein, refers to a nucleic acid or non-nucleic acid linker molecule that is designed as a biodegradable linker to connect one molecule to another molecule, for example, a biologically active molecule to a siNA molecule of the invention or the sense and antisense strands of a siNA molecule of the invention. The biodegradable linker is designed such that its stability can be modulated

for a particular purpose, such as delivery to a particular tissue or cell type. The stability of a nucleic acid-based biodegradable linker molecule can be modulated by using various chemistries, for example combinations of ribonucleotides, deoxyribonucleotides, and chemically-modified nucleotides, such as 2'-O-methyl, 2'-fluoro, 2'-amino, 2'-O-amino, 5 2'-C-allyl, 2'-O-allyl, and other 2'-modified or base modified nucleotides. The biodegradable nucleic acid linker molecule can be a dimer, trimer, tetramer or longer nucleic acid molecule, for example, an oligonucleotide of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length, or can comprise a single nucleotide with a phosphorus-based linkage, for example, a phosphoramidate or 10 phosphodiester linkage. The biodegradable nucleic acid linker molecule can also comprise nucleic acid backbone, nucleic acid sugar, or nucleic acid base modifications.

The term "biodegradable" as used herein, refers to degradation in a biological system, for example enzymatic degradation or chemical degradation.

The term "biologically active molecule" as used herein, refers to compounds or 15 molecules that are capable of eliciting or modifying a biological response in a system. Non-limiting examples of biologically active siNA molecules either alone or in combination with other molecules contemplated by the instant invention include therapeutically active molecules such as antibodies, cholesterol, hormones, antivirals, peptides, proteins, chemotherapeutics, small molecules, vitamins, co-factors, 20 nucleosides, nucleotides, oligonucleotides, enzymatic nucleic acids, antisense nucleic acids, triplex forming oligonucleotides, 2,5-A chimeras, siNA, dsRNA, allozymes, aptamers, decoys and analogs thereof. Biologically active molecules of the invention also include molecules capable of modulating the pharmacokinetics and/or pharmacodynamics of other biologically active molecules, for example, lipids and 25 polymers such as polyamines, polyamides, polyethylene glycol and other polyethers.

The term "phospholipid" as used herein, refers to a hydrophobic molecule comprising at least one phosphorus group. For example, a phospholipid can comprise a phosphorus-containing group and saturated or unsaturated alkyl group, optionally substituted with OH, COOH, oxo, amine, or substituted or unsubstituted aryl groups.

Therapeutic nucleic acid molecules (*e.g.*, siNA molecules) delivered exogenously optimally are stable within cells until reverse transcription of the RNA has been modulated long enough to reduce the levels of the RNA transcript. The nucleic acid molecules are resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

In yet another embodiment, siNA molecules having chemical modifications that maintain or enhance enzymatic activity of proteins involved in RNAi are provided. Such nucleic acids are also generally more resistant to nucleases than unmodified nucleic acids. Thus, *in vitro* and/or *in vivo* the activity should not be significantly lowered.

Use of the nucleic acid-based molecules of the invention will lead to better treatment of the disease progression by affording the possibility of combination therapies (*e.g.*, multiple siNA molecules targeted to different genes; nucleic acid molecules coupled with known small molecule modulators; or intermittent treatment with combinations of molecules, including different motifs and/or other chemical or biological molecules). The treatment of subjects with siNA molecules can also include combinations of different types of nucleic acid molecules, such as enzymatic nucleic acid molecules (ribozymes), allozymes, antisense, 2,5-A oligoadenylate, decoys, and aptamers.

In another aspect a siNA molecule of the invention comprises one or more 5' and/or a 3'- cap structure, for example on only the sense siNA strand, the antisense siNA strand, or both siNA strands.

By "cap structure" is meant chemical modifications, which have been incorporated at either terminus of the oligonucleotide (see, for example, Adamic *et al.*, U.S. Pat. No. 5,998,203, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-terminal (3'-cap) or may be present on both termini. In non-limiting examples, the 5'-cap

includes, but is not limited to, glyceryl, inverted deoxy abasic residue (moiety); 4',5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide, 4'-thio nucleotide; carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuransyl nucleotide; 5 acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging 10 methylphosphonate moiety.

Non-limiting examples of the 3'-cap include, but are not limited to, glyceryl, inverted deoxy abasic residue (moiety), 4', 5'-methylene nucleotide; 1-(beta-D-erythrofuransyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate; 3-aminopropyl phosphate; 6-aminohexyl 15 phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuransyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4- 20 butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein).

By the term "non-nucleotide" is meant any group or compound which can be 25 incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine and therefore lacks a base at the 1'-position.

30 An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12

carbons. More preferably, it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂ or N(CH₃)₂, amino, or SH. The term also includes alkenyl groups that are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably, it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂, halogen, N(CH₃)₂, amino, or SH. The term "alkyl" also includes alkynyl groups that have an unsaturated hydrocarbon group containing at least one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably, it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group may be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =O, =S, NO₂ or N(CH₃)₂, amino or SH.

Such alkyl groups can also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group that has at least one ring having a conjugated pi electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which may be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyridyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

By "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see, for example, Usman and McSwiggen, *supra*; Eckstein *et al.*, International PCT Publication No. WO 92/07065; Usman *et al.*, International PCT Publication No. WO 93/15187; Uhlman & Peyman, *supra*, all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach *et al.*, 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-limiting examples of base modifications that can be introduced into nucleic acid molecules include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (*e.g.*, 5-methylcytidine), 5-alkyluridines (*e.g.*, ribothymidine), 5-halouridine (*e.g.*, 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (*e.g.* 6-methyluridine), propyne, and others (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090; Uhlman & Peyman, *supra*). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents.

In one embodiment, the invention features modified siNA molecules, with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, phosphotriester, morpholino, amidate carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications, see Hunziker and Leumann, 1995, *Nucleic Acid Analogues: Synthesis and Properties*, in *Modern Synthetic Methods*, VCH, 331-417, and Mesmaeker *et al.*, 1994, *Novel Backbone Replacements for Oligonucleotides*, in *Carbohydrate Modifications in Antisense Research*, ACS, 24-39.

By "abasic" is meant sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position, see for example Adamic *et al.*, U.S. Pat. No. 5,998,203.

By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, thymine, or uracil joined to the 1' carbon of β -D-ribo-furanose.

By "modified nucleoside" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate. Non-limiting examples of modified nucleotides are shown by Formulae I-VII and/or other modifications described herein.

In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'-NH₂ or 2'-O- NH₂, which can be modified or unmodified. Such modified groups are described, for example, in Eckstein *et al.*, U.S. Pat. No. 5,672,695 and Matulic-Adamic *et al.*, U.S. Pat. No. 6,248,878, which are both incorporated by reference in their entireties.

Various modifications to nucleic acid siNA structure can be made to enhance the utility of these molecules. Such modifications will enhance shelf-life, half-life *in vitro*, stability, and ease of introduction of such oligonucleotides to the target site, *e.g.*, to enhance penetration of cellular membranes, and confer the ability to recognize and bind to targeted cells.

Administration of Nucleic Acid Molecules

A siNA molecule of the invention can be adapted for use to treat, for example, Huntington disease and related conditions such as progressive chorea, rigidity, dementia, and seizures, spinocerebellar ataxia, spinal and bulbar muscular dystrophy (SBMA), dentatorubropallidoluysian atrophy (DRPLA) and any other diseases or conditions that are related to or will respond to the levels of a repeat expansion (RE) gene in a cell or tissue, alone or in combination with other therapies. For example, a siNA molecule can comprise a delivery vehicle, including liposomes, for administration to a subject, carriers and diluents and their salts, and/or can be present in pharmaceutically acceptable formulations. Methods for the delivery of nucleic acid molecules are described in Akhtar *et al.*, 1992, *Trends Cell Bio.*, 2, 139; *Delivery Strategies for Antisense Oligonucleotide Therapeutics*, ed. Akhtar, 1995, Maurer *et al.*, 1999, *Mol. Membr. Biol.*, 16, 129-140; Hofland and Huang, 1999, *Handb. Exp. Pharmacol.*, 137, 165-192; and Lee

et al., 2000, *ACS Symp. Ser.*, 752, 184-192, all of which are incorporated herein by reference. Beigelman *et al.*, U.S. Pat. No. 6,395,713 and Sullivan *et al.*, PCT WO 94/02595 further describe the general methods for delivery of nucleic acid molecules. These protocols can be utilized for the delivery of virtually any nucleic acid molecule.

5 Nucleic acid molecules can be administered to cells by a variety of methods known to those of skill in the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as biodegradable polymers, hydrogels, cyclodextrins (see for example Gonzalez *et al.*, 1999, *Bioconjugate Chem.*, 10, 1068-1074; Wang *et al.*, International PCT publication Nos. WO 03/47518 and WO

10 03/46185), poly(lactic-co-glycolic)acid (PLGA) and PLCA microspheres (see for example US Patent 6,447,796 and US Patent Application Publication No. US 2002130430), biodegradable nanocapsules, and bioadhesive microspheres, or by proteinaceous vectors (O'Hare and Normand, International PCT Publication No. WO 00/53722). In another embodiment, the nucleic acid molecules of the invention can also

15 be formulated or complexed with polyethyleneimine and derivatives thereof, such as polyethyleneimine-polyethyleneglycol-N-acetylgalactosamine (PEI-PEG-GAL) or polyethyleneimine-polyethyleneglycol-tri-N-acetylgalactosamine (PEI-PEG-triGAL) derivatives. Alternatively, the nucleic acid/vehicle combination is locally delivered by direct injection or by use of an infusion pump. Many examples in the art describe CNS

20 delivery methods of oligonucleotides by osmotic pump, (see Chun *et al.*, 1998, *Neuroscience Letters*, 257, 135-138, D'Aldin *et al.*, 1998, *Mol. Brain Research*, 55, 151-164, Dryden *et al.*, 1998, *J. Endocrinol.*, 157, 169-175, Ghirnikar *et al.*, 1998, *Neuroscience Letters*, 247, 21-24) or direct infusion (Broaddus *et al.*, 1997, *Neurosurg. Focus*, 3, article 4). Various devices as are known in the art can be utilized to deliver

25 nucleic acid molecules of the invention (see for example Turner, 2003, *Acta Neurochir Suppl.*, 87, 29-35). Other routes of delivery include, but are not limited to oral (tablet or pill form) and/or intrathecal delivery (Gold, 1997, *Neuroscience*, 76, 1153-1158). For a comprehensive review on drug delivery strategies including broad coverage of CNS delivery, see Ho *et al.*, 1999, *Curr. Opin. Mol. Ther.*, 1, 336-343 and Jain, *Drug Delivery*

30 *Systems: Technologies and Commercial Opportunities*, Decision Resources, 1998 and Groothuis *et al.*, 1997, *J. NeuroVirol.*, 3, 387-400. Direct injection of the nucleic acid molecules of the invention, whether subcutaneous, intramuscular, or intradermal, can

take place using standard needle and syringe methodologies, or by needle-free technologies such as those described in Conry *et al.*, 1999, *Clin. Cancer Res.*, 5, 2330-2337 and Barry *et al.*, International PCT Publication No. WO 99/31262. The molecules of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents
 5 prevent, modulate the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a subject.

Experiments have demonstrated the efficient *in vivo* uptake of nucleic acids by neurons. As an example of local administration of nucleic acids to nerve cells, Sommer *et al.*, 1998, *Antisense Nuc. Acid Drug Dev.*, 8, 75, describe a study in which a 15mer
 10 phosphorothioate antisense nucleic acid molecule to c-fos is administered to rats via microinjection into the brain. Antisense molecules labeled with tetramethylrhodamine-isothiocyanate (TRITC) or fluorescein isothiocyanate (FITC) were taken up by exclusively by neurons thirty minutes post-injection. A diffuse cytoplasmic staining and nuclear staining was observed in these cells. As an example of systemic administration
 15 of nucleic acid to nerve cells, Epa *et al.*, 2000, *Antisense Nuc. Acid Drug Dev.*, 10, 469, describe an *in vivo* mouse study in which beta-cyclodextrin-adamantane-oligonucleotide conjugates were used to target the p75 neurotrophin receptor in neuronally differentiated PC12 cells. Following a two week course of IP administration, pronounced uptake of p75 neurotrophin receptor antisense was observed in dorsal root ganglion (DRG) cells.
 20 In addition, a marked and consistent down-regulation of p75 was observed in DRG neurons. Additional approaches to the targeting of nucleic acid to neurons are described in Broaddus *et al.*, 1998, *J. Neurosurg.*, 88(4), 734; Karle *et al.*, 1997, *Eur. J. Pharmacol.*, 340(2/3), 153; Bannai *et al.*, 1998, *Brain Research*, 784(1,2), 304; Rajakumar *et al.*, 1997, *Synapse*, 26(3), 199; Wu-pong *et al.*, 1999, *BioPharm*, 12(1), 32;
 25 Bannai *et al.*, 1998, *Brain Res. Protoc.*, 3(1), 83; Simantov *et al.*, 1996, *Neuroscience*, 74(1), 39. Nucleic acid molecules of the invention are therefore amenable to delivery to and uptake by cells that express repeat expansion allelic variants for modulation of RE gene expression.

The delivery of nucleic acid molecules of the invention, targeting RE is provided
 30 by a variety of different strategies. Traditional approaches to CNS delivery that can be used include, but are not limited to, intrathecal and intracerebroventricular

administration, implantation of catheters and pumps, direct injection or perfusion at the site of injury or lesion, injection into the brain arterial system, or by chemical or osmotic opening of the blood-brain barrier. Other approaches can include the use of various transport and carrier systems, for example though the use of conjugates and
5 biodegradable polymers. Furthermore, gene therapy approaches, for example as described in Kaplitt *et al.*, US 6,180,613 and Davidson, WO 04/013280, can be used to express nucleic acid molecules in the CNS.

In one embodiment, a siNA molecule of the invention is complexed with membrane disruptive agents such as those described in U.S. Patent Appliaction
10 Publication No. 20010007666, incorporated by reference herein in its entirety including the drawings. In another embodiment, the membrane disruptive agent or agents and the siNA molecule are also complexed with a cationic lipid or helper lipid molecule, such as those lipids described in U.S. Patent No. 6,235,310, incorporated by reference herein in its entirety including the drawings.

15 Thus, the invention features a pharmaceutical composition comprising one or more nucleic acid(s) of the invention in an acceptable carrier, such as a stabilizer, buffer, and the like. The polynucleotides of the invention can be administered (*e.g.*, RNA, DNA or protein) and introduced into a subject by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a
20 liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention can also be formulated and used as tablets, capsules or elixirs for oral administration, suppositories for rectal administration, sterile solutions, suspensions for injectable administration, and the other compositions known in the art.

25 The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds, *e.g.*, acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

A pharmacological composition or formulation refers to a composition or
30 formulation in a form suitable for administration, *e.g.*, systemic administration, into a

cell or subject, including for example a human. Suitable forms, in part, depend upon the use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation from reaching a target cell (*i.e.*, a cell to which the negatively charged nucleic acid is desirable for delivery). For example,
5 pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms that prevent the composition or formulation from exerting its effect.

By "systemic administration" is meant *in vivo* systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body.
10 Administration routes that lead to systemic absorption include, without limitation: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes exposes the siNA molecules of the invention to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a
15 liposome or other drug carrier comprising the compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation that can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach can provide enhanced delivery of the drug to target cells by
20 taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as cells producing excess repeat expansion genes.

By "pharmaceutically acceptable formulation" is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention in the physical location most suitable for their desired activity. Non-
25 limiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: P-glycoprotein inhibitors (such as Pluronic P85), which can enhance entry of drugs into the CNS (Joliet-Riant and Tillement, 1999, *Fundam. Clin. Pharmacol.*, 13, 16-26); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after intracerebral implantation (Emerich, DF
30 *et al*, 1999, *Cell Transplant*, 8, 47-58) (Alkermes, Inc. Cambridge, MA); and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs

across the blood brain barrier and can alter neuronal uptake mechanisms (*Prog Neuropsychopharmacol Biol Psychiatry*, 23, 941-949, 1999). Other non-limiting examples of delivery strategies for the nucleic acid molecules of the instant invention include material described in Boado *et al.*, 1998, *J. Pharm. Sci.*, 87, 1308-1315; Tyler *et al.*, 1999, *FEBS Lett.*, 421, 280-284; Pardridge *et al.*, 1995, *PNAS USA.*, 92, 5592-5596; Boado, 1995, *Adv. Drug Delivery Rev.*, 15, 73-107; Aldrian-Herrada *et al.*, 1998, *Nucleic Acids Res.*, 26, 4910-4916; and Tyler *et al.*, 1999, *PNAS USA.*, 96, 7053-7058.

The invention also features the use of the composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic *et al. Chem. Rev.* 1995, 95, 2601-2627; Ishiwata *et al., Chem. Pharm. Bull.* 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic *et al., Science* 1995, 267, 1275-1276; Oku *et al., 1995, Biochim. Biophys. Acta*, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu *et al., J. Biol. Chem.* 1995, 270, 24864-24870; Choi *et al.*, International PCT Publication No. WO 96/10391; Ansell *et al.*, International PCT Publication No. WO 96/10390; Holland *et al.*, International PCT Publication No. WO 96/10392). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen.

The present invention also includes compositions prepared for storage or administration that include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R.

Gennaro edit. 1985), hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents can be provided. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents can be used.

5 A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent
10 medication, and other factors that those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

 The nucleic acid molecules of the invention and formulations thereof can be administered orally, topically, parenterally, by inhalation or spray, or rectally in dosage
15 unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants and/or vehicles. The term parenteral as used herein includes percutaneous, subcutaneous, intravascular (*e.g.*, intravenous), intramuscular, or intrathecal injection or infusion techniques and the like. In addition, there is provided a pharmaceutical formulation comprising a nucleic acid molecule of the invention and a
20 pharmaceutically acceptable carrier. One or more nucleic acid molecules of the invention can be present in association with one or more non-toxic pharmaceutically acceptable carriers and/or diluents and/or adjuvants, and if desired other active ingredients. The pharmaceutical compositions containing nucleic acid molecules of the invention can be in a form suitable for oral use, for example, as tablets, troches,
25 lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsion, hard or soft capsules, or syrups or elixirs.

 Compositions intended for oral use can be prepared according to any method known to the art for the manufacture of pharmaceutical compositions and such compositions can contain one or more such sweetening agents, flavoring agents, coloring
30 agents or preservative agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic

pharmaceutically acceptable excipients that are suitable for the manufacture of tablets. These excipients can be, for example, inert diluents; such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for example starch, gelatin or acacia; and lubricating agents, for example magnesium stearate, stearic acid or talc. The tablets can be uncoated or they can be coated by known techniques. In some cases such coatings can be prepared by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained action over a longer period. For example, a time delay material such as glyceryl monostearate or glyceryl distearate can be employed.

Formulations for oral use can also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium, for example peanut oil, liquid paraffin or olive oil.

Aqueous suspensions contain the active materials in a mixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydropropylmethylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents can be a naturally-occurring phosphatide, for example, lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate, or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethyleneoxycetanol, or condensation products of ethylene oxide with partial esters derived from fatty acids and a hexitol such as polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with partial esters derived from fatty acids and hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions can also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents, and one or more sweetening agents, such as sucrose or saccharin.

Oily suspensions can be formulated by suspending the active ingredients in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in a mineral

oil such as liquid paraffin. The oily suspensions can contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents and flavoring agents can be added to provide palatable oral preparations. These compositions can be preserved by the addition of an anti-oxidant such as ascorbic acid

5 Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents or suspending agents are exemplified by those already mentioned above. Additional excipients, for example sweetening, flavoring and coloring
10 agents, can also be present.

 Pharmaceutical compositions of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil or mixtures of these. Suitable emulsifying agents can be naturally-occurring gums, for example gum acacia or gum tragacanth, naturally-occurring phosphatides, for example soy bean,
15 lecithin, and esters or partial esters derived from fatty acids and hexitol, anhydrides, for example sorbitan monooleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monooleate. The emulsions can also contain sweetening and flavoring agents.

 Syrups and elixirs can be formulated with sweetening agents, for example glycerol,
20 propylene glycol, sorbitol, glucose or sucrose. Such formulations can also contain a demulcent, a preservative and flavoring and coloring agents. The pharmaceutical compositions can be in the form of a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents that have been mentioned above.
25 The sterile injectable preparation can also be a sterile injectable solution or suspension in a non-toxic parentally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that can be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any
30 bland fixed oil can be employed including synthetic mono-or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

The nucleic acid molecules of the invention can also be administered in the form of suppositories, *e.g.*, for rectal administration of the drug. These compositions can be prepared by mixing the drug with a suitable non-irritating excipient that is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include cocoa butter and polyethylene glycols.

Nucleic acid molecules of the invention can be administered parenterally in a sterile medium. The drug, depending on the vehicle and concentration used, can either be suspended or dissolved in the vehicle. Advantageously, adjuvants such as local anesthetics, preservatives and buffering agents can be dissolved in the vehicle.

Dosage levels of the order of from about 0.1 mg to about 140 mg per kilogram of body weight per day are useful in the treatment of the above-indicated conditions (about 0.5 mg to about 7 g per subject per day). The amount of active ingredient that can be combined with the carrier materials to produce a single dosage form varies depending upon the host treated and the particular mode of administration. Dosage unit forms generally contain between from about 1 mg to about 500 mg of an active ingredient.

It is understood that the specific dose level for any particular subject depends upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, sex, diet, time of administration, route of administration, and rate of excretion, drug combination and the severity of the particular disease undergoing therapy.

For administration to non-human animals, the composition can also be added to the animal feed or drinking water. It can be convenient to formulate the animal feed and drinking water compositions so that the animal takes in a therapeutically appropriate quantity of the composition along with its diet. It can also be convenient to present the composition as a premix for addition to the feed or drinking water.

The nucleic acid molecules of the present invention can also be administered to a subject in combination with other therapeutic compounds to increase the overall

therapeutic effect. The use of multiple compounds to treat an indication can increase the beneficial effects while reducing the presence of side effects.

In one embodiment, the invention comprises compositions suitable for administering nucleic acid molecules of the invention to specific cell types. For example, the asialoglycoprotein receptor (ASGPr) (Wu and Wu, 1987, *J. Biol. Chem.* 262, 4429-4432) is unique to hepatocytes and binds branched galactose-terminal glycoproteins, such as asialoorosomucoid (ASOR). In another example, the folate receptor is overexpressed in many cancer cells. Binding of such glycoproteins, synthetic glycoconjugates, or folates to the receptor takes place with an affinity that strongly depends on the degree of branching of the oligosaccharide chain, for example, triantennary structures are bound with greater affinity than biantennary or monoantennary chains (Baenziger and Fiete, 1980, *Cell*, 22, 611-620; Connolly *et al.*, 1982, *J. Biol. Chem.*, 257, 939-945). Lee and Lee, 1987, *Glycoconjugate J.*, 4, 317-328, obtained this high specificity through the use of N-acetyl-D-galactosamine as the carbohydrate moiety, which has higher affinity for the receptor, compared to galactose. This "clustering effect" has also been described for the binding and uptake of mannosyl-terminating glycoproteins or glycoconjugates (Ponpipom *et al.*, 1981, *J. Med. Chem.*, 24, 1388-1395). The use of galactose, galactosamine, or folate based conjugates to transport exogenous compounds across cell membranes can provide a targeted delivery approach to, for example, the treatment of liver disease, cancers of the liver, or other cancers. The use of bioconjugates can also provide a reduction in the required dose of therapeutic compounds required for treatment. Furthermore, therapeutic bioavailability, pharmacodynamics, and pharmacokinetic parameters can be modulated through the use of nucleic acid bioconjugates of the invention. Non-limiting examples of such bioconjugates are described in Vargeese *et al.*, USSN 10/201,394, filed August 13, 2001; and Matulic-Adamic *et al.*, USSN 10/151,116, filed May 17, 2002. In one embodiment, nucleic acid molecules of the invention are complexed with or covalently attached to nanoparticles, such as Hepatitis B virus S, M, or L envelope proteins (see for example Yamado *et al.*, 2003, *Nature Biotechnology*, 21, 885). In one embodiment, nucleic acid molecules of the invention are delivered with specificity for human tumor cells, specifically non-apoptotic human tumor cells including for example T-cells, hepatocytes, breast carcinoma cells, ovarian carcinoma cells, melanoma cells, intestinal epithelial

cells, prostate cells, testicular cells, non-small cell lung cancers, small cell lung cancers, etc.

Alternatively, certain siNA molecules of the instant invention can be expressed within cells from eukaryotic promoters (e.g., Izant and Weintraub, 1985, *Science*, 229, 345; McGarry and Lindquist, 1986, *Proc. Natl. Acad. Sci.*, USA 83, 399; Scanlon *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, 88, 10591-5; Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Dropulic *et al.*, 1992, *J. Virol.*, 66, 1432-41; Weerasinghe *et al.*, 1991, *J. Virol.*, 65, 5531-4; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. USA*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Sarver *et al.*, 1990 *Science*, 247, 1222-1225; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Good *et al.*, 1997, *Gene Therapy*, 4, 45. Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity of such nucleic acids can be augmented by their release from the primary transcript by a enzymatic nucleic acid (Draper *et al.*, PCT WO 93/23569, and Sullivan *et al.*, PCT WO 94/02595; Ohkawa *et al.*, 1992, *Nucleic Acids Symp. Ser.*, 27, 15-6; Taira *et al.*, 1991, *Nucleic Acids Res.*, 19, 5125-30; Ventura *et al.*, 1993, *Nucleic Acids Res.*, 21, 3249-55; Chowrira *et al.*, 1994, *J. Biol. Chem.*, 269, 25856.

In another aspect of the invention, RNA molecules of the present invention can be expressed from transcription units (see for example Couture *et al.*, 1996, *TIG.*, 12, 510) inserted into DNA or RNA vectors. The recombinant vectors can be DNA plasmids or viral vectors. siNA expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. In another embodiment, pol III based constructs are used to express nucleic acid molecules of the invention (see for example Thompson, U.S. Pats. Nos. 5,902,880 and 6,146,886). The recombinant vectors capable of expressing the siNA molecules can be delivered as described above, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of nucleic acid molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the siNA molecule interacts with the target mRNA and generates an RNAi response. Delivery of siNA molecule expressing vectors can be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from a subject followed by reintroduction into

the subject, or by any other means that would allow for introduction into the desired target cell (for a review see Couture *et al.*, 1996, *TIG.*, 12, 510).

In one aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one siNA molecule of the instant invention. The expression
5 vector can encode one or both strands of a siNA duplex, or a single self-complementary strand that self hybridizes into a siNA duplex. The nucleic acid sequences encoding the siNA molecules of the instant invention can be operably linked in a manner that allows expression of the siNA molecule (see for example Paul *et al.*, 2002, *Nature Biotechnology*, 19, 505; Miyagishi and Taira, 2002, *Nature Biotechnology*, 19, 497; Lee
10 *et al.*, 2002, *Nature Biotechnology*, 19, 500; and Novina *et al.*, 2002, *Nature Medicine*, advance online publication doi:10.1038/nm725).

In another aspect, the invention features an expression vector comprising: a) a transcription initiation region (*e.g.*, eukaryotic pol I, II or III initiation region); b) a transcription termination region (*e.g.*, eukaryotic pol I, II or III termination region); and
15 c) a nucleic acid sequence encoding at least one of the siNA molecules of the instant invention, wherein said sequence is operably linked to said initiation region and said termination region in a manner that allows expression and/or delivery of the siNA molecule. The vector can optionally include an open reading frame (ORF) for a protein operably linked on the 5' side or the 3'-side of the sequence encoding the siNA of the
20 invention; and/or an intron (intervening sequences).

Transcription of the siNA molecule sequences can be driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters are expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type depends on the nature
25 of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990, *Proc. Natl. Acad. Sci. U S A*, 87, 6743-7; Gao and Huang 1993, *Nucleic Acids Res.*, 21, 2867-72; Lieber *et al.*, 1993, *Methods Enzymol.*, 217, 47-66; Zhou *et al.*, 1990, *Mol.*
30 *Cell. Biol.*, 10, 4529-37). Several investigators have demonstrated that nucleic acid molecules expressed from such promoters can function in mammalian cells (*e.g.*

Kashani-Sabet *et al.*, 1992, *Antisense Res. Dev.*, 2, 3-15; Ojwang *et al.*, 1992, *Proc. Natl. Acad. Sci. U S A*, 89, 10802-6; Chen *et al.*, 1992, *Nucleic Acids Res.*, 20, 4581-9; Yu *et al.*, 1993, *Proc. Natl. Acad. Sci. U S A*, 90, 6340-4; L'Huillier *et al.*, 1992, *EMBO J.*, 11, 4411-8; Lisiewicz *et al.*, 1993, *Proc. Natl. Acad. Sci. U. S. A.*, 90, 8000-4; Thompson *et al.*, 1995, *Nucleic Acids Res.*, 23, 2259; Sullenger & Cech, 1993, *Science*, 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as siNA in cells (Thompson *et al.*, *supra*; Couture and Stinchcomb, 1996, *supra*; Noonberg *et al.*, 1994, *Nucleic Acid Res.*, 22, 2830; Noonberg *et al.*, U.S. Pat. No. 5,624,803; Good *et al.*, 1997, *Gene Ther.*, 4, 45; Beigelman *et al.*, International PCT Publication No. WO 96/18736. The above siNA transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, 1996, *supra*).

In another aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one of the siNA molecules of the invention in a manner that allows expression of that siNA molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; and c) a nucleic acid sequence encoding at least one strand of the siNA molecule, wherein the sequence is operably linked to the initiation region and the termination region in a manner that allows expression and/or delivery of the siNA molecule.

In another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; and d) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the open reading frame and the termination region in a manner that allows expression and/or delivery of the siNA molecule. In yet another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; and d) a

nucleic acid sequence encoding at least one siNA molecule, wherein the sequence is operably linked to the initiation region, the intron and the termination region in a manner which allows expression and/or delivery of the nucleic acid molecule.

In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; and e) a nucleic acid sequence encoding at least one strand of a siNA molecule, wherein the sequence is operably linked to the 3'-end of the open reading frame and wherein the sequence is operably linked to the initiation region, the intron, the open reading frame and the termination region in a manner which allows expression and/or delivery of the siNA molecule.

Huntingtin biology and biochemistry

The following discussion is adapted from the Revilla *et al.*, 2002, Huntington Disease, Copyright 2004, eMedicine.com, Inc. and the OMIM database entry for Huntington disease, Copyright © 1966-2004 Johns Hopkins University. Huntington disease (HD) is an incurable, adult-onset, autosomal dominant inherited disorder associated with cell loss within a specific subset of neurons in the basal ganglia and cortex. HD is named after George Huntington, the physician who described it as hereditary chorea in 1872. Characteristic features of HD include involuntary movements, dementia, and behavioral changes. Huntington disease (HD) is inherited as an autosomal dominant disease that gives rise to progressive, selective or localized neural cell death associated with choreic movements and dementia. The classic signs of Huntington disease are progressive chorea, rigidity, and dementia, often associated with seizures. A characteristic atrophy of the caudate nucleus is seen in radiographic images. The most striking neuropathology in HD occurs within the neostriatum, in which gross atrophy of the caudate nucleus and putamen is accompanied by selective neuronal loss and astrogliosis. Other regions, including the globus pallidus, thalamus, subthalamic nucleus, substantia nigra, and cerebellum, show varying degrees of atrophy depending on the pathologic grade. The extent of gross striatal pathology, neuronal loss, and gliosis provides a basis for grading the severity of HD pathology (grades 0-4). Typically, there is a prodromal phase of mild psychotic and behavioral symptoms which precedes frank Huntington chorea by up to 10 years.

The disease is associated with increases in the length of a polyglutamine or CAG triplet repeat present in the Huntingtin gene located on chromosome 4p16.3. The function of huntingtin is not known. Normally, it is located in the cytoplasm. The association of huntingtin with the cytoplasmic surface of a variety of organelles, including transport vesicles, synaptic vesicles, microtubules, and mitochondria, raises the possibility of the occurrence of normal cellular interactions that might be relevant to neurodegeneration. Although the variation in age at onset of HD is partly explained by the size of the expanded CAG repeat, it is strongly heritable, which suggests that other genes modify the age at onset.

Studies have shown that mutant huntingtin protein from human brain, transgenic animals, and cells is more resistant to proteolysis than normal huntingtin. The N-terminal cleavage fragments that arise from the processing of normal huntingtin are sequestered by full-length huntingtin. One model has been proposed in which inhibition of proteolysis of mutant huntingtin leads to aggregation and neurotoxicity through the sequestration of important targets, including normal huntingtin. The presence of neuronal intranuclear inclusions (NIIs) initially led to the view that they are toxic and, hence, pathogenic. More recent data from striatal neuronal cultures transfected with mutant huntingtin and transgenic mice carrying the spinocerebellar ataxia-1 (*SCA-1*) gene (another CAG repeat disorder) suggest that NIIs may not be necessary or sufficient to cause neuronal cell death, but translocation into the nucleus is sufficient to cause neuronal cell death. Caspase inhibition in clonal striatal cells showed no correlation between the reduction of aggregates in the cells and increased survival.

Cytoplasmic protein extracts from several rat brain regions, including striatum and cortex (sites of neuronal degeneration in HD), contain a 63 kD RNA-binding protein that interacts specifically with CAG repeat sequences. It has been noted that the protein RNA interactions are dependent upon the length of the CAG repeat, and that longer repeats bind substantially more protein. Two CAG binding proteins have been identified in human cortex and striatum, one of 63 kD and another of 49 kD. These data suggest mechanisms by which RNA binding proteins may be involved in the pathological course of trinucleotide-associated neurologic diseases (see for example McLaughlin *et al.*, 1996, *Hum. Genet.* 59, 561-569).

The Huntington's Disease Collaborative Research Group (1993, *Cell*, 72, 971-983) found a gene, designated IT15 (important transcript 15) and later called huntingtin, which was isolated using cloned trapped exons and which contains a polymorphic trinucleotide repeat that is expanded and unstable on HD chromosomes. A (CAG)_n repeat longer than the normal range was observed on HD chromosomes from all disease families examined. The families came from a variety of ethnic backgrounds and demonstrated a variety of 4p16.3 haplotypes. The (CAG)_n repeat appeared to be located within the coding sequence of a predicted protein of about 348 kD that is widely expressed but unrelated to any known gene. Thus, the HD mutation involves an unstable DNA segment similar to those previously observed in several disorders, including the fragile X syndrome, Kennedy syndrome, and myotonic dystrophy. The fact that the phenotype of HD is completely dominant suggests that the disorder results from a gain-of-function mutation in which either the mRNA product or the protein product of the disease allele has some new property or is expressed inappropriately (see for example, Myers *et al.*, 1989, *Am. J. Hum. Genet.*, 34, 481-488).

The use of small interfering nucleic acid molecules targeting HD, for example mutant alleles associated with Huntington disease, provides a class of novel therapeutic agents that can be used in the the treatment of Huntington Disease and any other disease or condition that responds to modulation of HD genes.

20 Examples:

The following are non-limiting examples showing the selection, isolation, synthesis and activity of nucleic acids of the instant invention.

Example 1: Tandem synthesis of siNA constructs

Exemplary siNA molecules of the invention are synthesized in tandem using a cleavable linker, for example, a succinyl-based linker. Tandem synthesis as described herein is followed by a one-step purification process that provides RNAi molecules in high yield. This approach is highly amenable to siNA synthesis in support of high throughput RNAi screening, and can be readily adapted to multi-column or multi-well synthesis platforms.

After completing a tandem synthesis of a siNA oligo and its complement in which the 5'-terminal dimethoxytrityl (5'-O-DMT) group remains intact (trityl on synthesis), the oligonucleotides are deprotected as described above. Following deprotection, the siNA sequence strands are allowed to spontaneously hybridize. This hybridization yields a duplex in which one strand has retained the 5'-O-DMT group while the complementary strand comprises a terminal 5'-hydroxyl. The newly formed duplex behaves as a single molecule during routine solid-phase extraction purification (Trityl-On purification) even though only one molecule has a dimethoxytrityl group. Because the strands form a stable duplex, this dimethoxytrityl group (or an equivalent group, such as other trityl groups or other hydrophobic moieties) is all that is required to purify the pair of oligos, for example, by using a C18 cartridge.

Standard phosphoramidite synthesis chemistry is used up to the point of introducing a tandem linker, such as an inverted deoxy abasic succinate or glyceryl succinate linker (see **Figure 1**) or an equivalent cleavable linker. A non-limiting example of linker coupling conditions that can be used includes a hindered base such as diisopropylethylamine (DIPA) and/or DMAP in the presence of an activator reagent such as Bromotripyrrolidinophosphoniumhexafluorophosphate (PyBrOP). After the linker is coupled, standard synthesis chemistry is utilized to complete synthesis of the second sequence leaving the terminal the 5'-O-DMT intact. Following synthesis, the resulting oligonucleotide is deprotected according to the procedures described herein and quenched with a suitable buffer, for example with 50mM NaOAc or 1.5M $\text{NH}_4\text{H}_2\text{CO}_3$.

Purification of the siNA duplex can be readily accomplished using solid phase extraction, for example using a Waters C18 SepPak 1g cartridge conditioned with 1 column volume (CV) of acetonitrile, 2 CV H_2O , and 2 CV 50mM NaOAc. The sample is loaded and then washed with 1 CV H_2O or 50mM NaOAc. Failure sequences are eluted with 1 CV 14% ACN (Aqueous with 50mM NaOAc and 50mM NaCl). The column is then washed, for example with 1 CV H_2O followed by on-column detritylation, for example by passing 1 CV of 1% aqueous trifluoroacetic acid (TFA) over the column, then adding a second CV of 1% aqueous TFA to the column and allowing to stand for approximately 10 minutes. The remaining TFA solution is removed and the column washed with H_2O followed by 1 CV 1M NaCl and additional

H₂O. The siNA duplex product is then eluted, for example, using 1 CV 20% aqueous CAN.

Figure 2 provides an example of MALDI-TOF mass spectrometry analysis of a purified siNA construct in which each peak corresponds to the calculated mass of an individual siNA strand of the siNA duplex. The same purified siNA provides three peaks when analyzed by capillary gel electrophoresis (CGE), one peak presumably corresponding to the duplex siNA, and two peaks presumably corresponding to the separate siNA sequence strands. Ion exchange HPLC analysis of the same siNA contract only shows a single peak. Testing of the purified siNA construct using a luciferase reporter assay described below demonstrated the same RNAi activity compared to siNA constructs generated from separately synthesized oligonucleotide sequence strands.

Example 2: Identification of potential siNA target sites in any RNA sequence

The sequence of an RNA target of interest, such as a viral or human mRNA transcript, is screened for target sites, for example by using a computer folding algorithm. In a non-limiting example, the sequence of a gene or RNA gene transcript derived from a database, such as Genbank, is used to generate siNA targets having complementarity to the target. Such sequences can be obtained from a database, or can be determined experimentally as known in the art. Target sites that are known, for example, those target sites determined to be effective target sites based on studies with other nucleic acid molecules, for example ribozymes or antisense, or those targets known to be associated with a disease or condition such as those sites containing mutations or deletions, can be used to design siNA molecules targeting those sites. Various parameters can be used to determine which sites are the most suitable target sites within the target RNA sequence. These parameters include but are not limited to secondary or tertiary RNA structure, the nucleotide base composition of the target sequence, the degree of homology between various regions of the target sequence, or the relative position of the target sequence within the RNA transcript. Based on these determinations, any number of target sites within the RNA transcript can be chosen to screen siNA molecules for efficacy, for example by using *in vitro* RNA cleavage assays, cell culture, or animal models. In a non-limiting example, anywhere from 1 to 1000 target sites are chosen within the transcript based on the size of the siNA construct to be

used. High throughput screening assays can be developed for screening siNA molecules using methods known in the art, such as with multi-well or multi-plate assays to determine efficient reduction in target gene expression.

Example 3: Selection of siNA molecule target sites in a RNA

5 The following non-limiting steps can be used to carry out the selection of siNAs targeting a given gene sequence or transcript.

1. The target sequence is parsed *in silico* into a list of all fragments or subsequences of a particular length, for example 23 nucleotide fragments, contained within the target sequence. This step is typically carried out using a custom Perl script, but
10 commercial sequence analysis programs such as Oligo, MacVector, or the GCG Wisconsin Package can be employed as well.
2. In some instances the siNAs correspond to more than one target sequence; such would be the case for example in targeting different transcripts of the same gene, targeting different transcripts of more than one gene, or for targeting both the human
15 gene and an animal homolog. In this case, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find matching sequences in each list. The subsequences are then ranked according to the number of target sequences that contain the given subsequence; the goal is to find subsequences that are present in most or all of the target sequences. Alternately, the ranking can
20 identify subsequences that are unique to a target sequence, such as a mutant target sequence. Such an approach would enable the use of siNA to target specifically the mutant sequence and not effect the expression of the normal sequence.
3. In some instances the siNA subsequences are absent in one or more sequences while present in the desired target sequence; such would be the case if the siNA targets a
25 gene with a paralogous family member that is to remain untargeted. As in case 2 above, a subsequence list of a particular length is generated for each of the targets, and then the lists are compared to find sequences that are present in the target gene but are absent in the untargeted paralog.

4. The ranked siNA subsequences can be further analyzed and ranked according to GC content. A preference can be given to sites containing 30-70% GC, with a further preference to sites containing 40-60% GC.
5. The ranked siNA subsequences can be further analyzed and ranked according to self-folding and internal hairpins. Weaker internal folds are preferred; strong hairpin structures are to be avoided.
6. The ranked siNA subsequences can be further analyzed and ranked according to whether they have runs of GGG or CCC in the sequence. GGG (or even more Gs) in either strand can make oligonucleotide synthesis problematic and can potentially interfere with RNAi activity, so it is avoided whenever better sequences are available. CCC is searched in the target strand because that will place GGG in the antisense strand.
7. The ranked siNA subsequences can be further analyzed and ranked according to whether they have the dinucleotide UU (uridine dinucleotide) on the 3'-end of the sequence, and/or AA on the 5'-end of the sequence (to yield 3' UU on the antisense sequence). These sequences allow one to design siNA molecules with terminal TT thymidine dinucleotides.
8. Four or five target sites are chosen from the ranked list of subsequences as described above. For example, in subsequences having 23 nucleotides, the right 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the upper (sense) strand of the siNA duplex, while the reverse complement of the left 21 nucleotides of each chosen 23-mer subsequence are then designed and synthesized for the lower (antisense) strand of the siNA duplex (see **Tables II and III**). If terminal TT residues are desired for the sequence (as described in paragraph 7), then the two 3' terminal nucleotides of both the sense and antisense strands are replaced by TT prior to synthesizing the oligos.
9. The siNA molecules are screened in an *in vitro*, cell culture or animal model system to identify the most active siNA molecule or the most preferred target site within the target RNA sequence.

10. Other design considerations can be used when selecting target nucleic acid sequences, see for example Reynolds *et al.*, 2004, *Nature Biotechnology Advanced Online Publication*, 1 February 2004, doi:10.1038/nbt936 and Ui-Tei *et al.*, 2004, *Nucleic Acids Research*, 32, doi:10.1093/nar/gkh247.

5 In an alternate approach, a pool of siNA constructs specific to a HD target sequence is used to screen for target sites in cells expressing HD RNA, such as COS-1 cells (see for example Sittler *et al.*, 2001, *Human Molecular Genetics*, 10, 1307-1315). The general strategy used in this approach is shown in **Figure 9**. A non-limiting example of such is a pool comprising sequences having any of SEQ ID NOS 1-3577.
 10 Cells expressing HD (e.g., COS-1 or PC12 cells) are transfected with the pool of siNA constructs and cells that demonstrate a phenotype associated with HD inhibition are sorted. The pool of siNA constructs can be expressed from transcription cassettes inserted into appropriate vectors (see for example **Figure 7** and **Figure 8**). The siNA from cells demonstrating a positive phenotypic change (e.g., decreased proliferation,
 15 decreased HD mRNA levels or decreased HD protein expression), are sequenced to determine the most suitable target site(s) within the target HD RNA sequence.

Example 4: HD targeted siNA design

siNA target sites were chosen by analyzing sequences of the HD RNA target and optionally prioritizing the target sites on the basis of folding (structure of any given
 20 sequence analyzed to determine siNA accessibility to the target), by using a library of siNA molecules as described in Example 3, or alternately by using an *in vitro* siNA system as described in Example 6 herein. siNA molecules were designed that could bind each target and are optionally individually analyzed by computer folding to assess whether the siNA molecule can interact with the target sequence. Varying the length of
 25 the siNA molecules can be chosen to optimize activity. Generally, a sufficient number of complementary nucleotide bases are chosen to bind to, or otherwise interact with, the target RNA, but the degree of complementarity can be modulated to accommodate siNA duplexes or varying length or base composition. By using such methodologies, siNA molecules can be designed to target sites within any known RNA sequence, for example
 30 those RNA sequences corresponding to the any gene transcript.

Chemically modified siNA constructs are designed to provide nuclease stability for systemic administration in vivo and/or improved pharmacokinetic, localization, and delivery properties while preserving the ability to mediate RNAi activity. Chemical modifications as described herein are introduced synthetically using synthetic methods described herein and those generally known in the art. The synthetic siNA constructs are then assayed for nuclease stability in serum and/or cellular/tissue extracts (e.g. liver extracts). The synthetic siNA constructs are also tested in parallel for RNAi activity using an appropriate assay, such as a luciferase reporter assay as described herein or another suitable assay that can quantify RNAi activity. Synthetic siNA constructs that possess both nuclease stability and RNAi activity can be further modified and re-evaluated in stability and activity assays. The chemical modifications of the stabilized active siNA constructs can then be applied to any siNA sequence targeting any chosen RNA and used, for example, in target screening assays to pick lead siNA compounds for therapeutic development (see for example **Figure 11**).

Example 5: Chemical Synthesis and Purification of siNA

siNA molecules can be designed to interact with various sites in the RNA message, for example, target sequences within the RNA sequences described herein. The sequence of one strand of the siNA molecule(s) is complementary to the target site sequences described above. The siNA molecules can be chemically synthesized using methods described herein. Inactive siNA molecules that are used as control sequences can be synthesized by scrambling the sequence of the siNA molecules such that it is not complementary to the target sequence. Generally, siNA constructs can be synthesized using solid phase oligonucleotide synthesis methods as described herein (see for example Usman *et al.*, US Patent Nos. 5,804,683; 5,831,071; 5,998,203; 6,117,657; 6,353,098; 6,362,323; 6,437,117; 6,469,158; Scaringe *et al.*, US Patent Nos. 6,111,086; 6,008,400; 6,111,086 all incorporated by reference herein in their entirety).

In a non-limiting example, RNA oligonucleotides are synthesized in a stepwise fashion using the phosphoramidite chemistry as is known in the art. Standard phosphoramidite chemistry involves the use of nucleosides comprising any of 5'-O-dimethoxytrityl, 2'-O-tert-butyldimethylsilyl, 3'-O-2-Cyanoethyl N,N-diisopropylphosphoroamidite groups, and exocyclic amine protecting groups (e.g. N6-benzoyl adenosine,

N4 acetyl cytidine, and N2-isobutyryl guanosine). Alternately, 2'-O-Silyl Ethers can be used in conjunction with acid-labile 2'-O-orthoester protecting groups in the synthesis of RNA as described by Scaringe *supra*. Differing 2' chemistries can require different protecting groups, for example 2'-deoxy-2'-amino nucleosides can utilize N-phthaloyl protection as described by Usman *et al.*, US Patent 5,631,360, incorporated by reference
5 herein in its entirety).

During solid phase synthesis, each nucleotide is added sequentially (3'- to 5'- direction) to the solid support-bound oligonucleotide. The first nucleoside at the 3'-end of the chain is covalently attached to a solid support (e.g., controlled pore glass or polystyrene) using various linkers. The nucleotide precursor, a ribonucleoside
10 phosphoramidite, and activator are combined resulting in the coupling of the second nucleoside phosphoramidite onto the 5'-end of the first nucleoside. The support is then washed and any unreacted 5'-hydroxyl groups are capped with a capping reagent such as acetic anhydride to yield inactive 5'-acetyl moieties. The trivalent phosphorus linkage is then oxidized to a more stable phosphate linkage. At the end of the nucleotide addition
15 cycle, the 5'-O-protecting group is cleaved under suitable conditions (e.g., acidic conditions for trityl-based groups and Fluoride for silyl-based groups). The cycle is repeated for each subsequent nucleotide.

Modification of synthesis conditions can be used to optimize coupling efficiency, for example by using differing coupling times, differing reagent/phosphoramidite concentrations, differing contact times, differing solid supports and solid support linker chemistries depending on the particular chemical composition of the siNA to be synthesized. Deprotection and purification of the siNA can be performed as is generally described in Deprotection and purification of the siNA can be performed as is generally
25 described in Usman *et al.*, US 5,831,071, US 6,353,098, US 6,437,117, and Bellon *et al.*, US 6,054,576, US 6,162,909, US 6,303,773, or Scaringe *supra*, incorporated by reference herein in their entireties. Additionally, deprotection conditions can be modified to provide the best possible yield and purity of siNA constructs. For example, applicant has observed that oligonucleotides comprising 2'-deoxy-2'-fluoro nucleotides
30 can degrade under inappropriate deprotection conditions. Such oligonucleotides are deprotected using aqueous methylamine at about 35°C for 30 minutes. If the 2'-deoxy-

2'-fluoro containing oligonucleotide also comprises ribonucleotides, after deprotection with aqueous methylamine at about 35°C for 30 minutes, TEA-HF is added and the reaction maintained at about 65°C for an additional 15 minutes.

Example 6: RNAi *in vitro* assay to assess siNA activity

5 An *in vitro* assay that recapitulates RNAi in a cell-free system is used to evaluate siNA constructs targeting HD RNA targets. The assay comprises the system described by Tuschl *et al.*, 1999, *Genes and Development*, 13, 3191-3197 and Zamore *et al.*, 2000, *Cell*, 101, 25-33 adapted for use with HD target RNA. A *Drosophila* extract derived from syncytial blastoderm is used to reconstitute RNAi activity *in vitro*. Target RNA is
10 generated via *in vitro* transcription from an appropriate HD expressing plasmid using T7 RNA polymerase or via chemical synthesis as described herein. Sense and antisense siNA strands (for example 20 uM each) are annealed by incubation in buffer (such as 100 mM potassium acetate, 30 mM HEPES-KOH, pH 7.4, 2 mM magnesium acetate) for 1 minute at 90°C followed by 1 hour at 37°C, then diluted in lysis buffer (for example
15 100 mM potassium acetate, 30 mM HEPES-KOH at pH 7.4, 2mM magnesium acetate). Annealing can be monitored by gel electrophoresis on an agarose gel in TBE buffer and stained with ethidium bromide. The *Drosophila* lysate is prepared using zero to two-hour-old embryos from Oregon R flies collected on yeasted molasses agar that are dechorionated and lysed. The lysate is centrifuged and the supernatant isolated. The
20 assay comprises a reaction mixture containing 50% lysate [vol/vol], RNA (10-50 pM final concentration), and 10% [vol/vol] lysis buffer containing siNA (10 nM final concentration). The reaction mixture also contains 10 mM creatine phosphate, 10 ug/ml creatine phosphokinase, 100 uM GTP, 100 uM UTP, 100 uM CTP, 500 uM ATP, 5 mM DTT, 0.1 U/uL RNasin (Promega), and 100 uM of each amino acid. The final
25 concentration of potassium acetate is adjusted to 100 mM. The reactions are pre-assembled on ice and preincubated at 25° C for 10 minutes before adding RNA, then incubated at 25° C for an additional 60 minutes. Reactions are quenched with 4 volumes of 1.25 x Passive Lysis Buffer (Promega). Target RNA cleavage is assayed by RT-PCR analysis or other methods known in the art and are compared to control reactions in
30 which siNA is omitted from the reaction.

Alternately, internally-labeled target RNA for the assay is prepared by *in vitro* transcription in the presence of [α - 32 P] CTP, passed over a G 50 Sephadex column by spin chromatography and used as target RNA without further purification. Optionally, target RNA is 5'- 32 P-end labeled using T4 polynucleotide kinase enzyme.

5 Assays are performed as described above and target RNA and the specific RNA cleavage products generated by RNAi are visualized on an autoradiograph of a gel. The percentage of cleavage is determined by Phosphor Imager[®] quantitation of bands representing intact control RNA or RNA from control reactions without siNA and the cleavage products generated by the assay.

10 In one embodiment, this assay is used to determine target sites the HD RNA target for siNA mediated RNAi cleavage, wherein a plurality of siNA constructs are screened for RNAi mediated cleavage of the HD RNA target, for example, by analyzing the assay reaction by electrophoresis of labeled target RNA, or by northern blotting, as well as by other methodology well known in the art.

15 Example 7: Nucleic acid inhibition of HD target RNA *in vitro*

siNA molecules targeted to the human HD RNA are designed and synthesized as described above. These nucleic acid molecules can be tested for cleavage activity *in vivo*, for example, using the following procedure. The target sequences and the nucleotide location within the HD RNA are given in **Table II and III**.

20 Two formats are used to test the efficacy of siNAs targeting HD. First, the reagents are tested in cell culture using, for example, COS-1, PC12 or A375 cells to determine the extent of RNA and protein inhibition. siNA reagents (*e.g.*; see **Tables II and III**) are selected against the HD target as described herein. RNA inhibition is measured after delivery of these reagents by a suitable transfection agent to, for example,

25 COS-1, PC12 or A375 cells. Relative amounts of target RNA are measured versus actin using real-time PCR monitoring of amplification (*eg.*, ABI 7700 Taqman[®]). A comparison is made to a mixture of oligonucleotide sequences made to unrelated targets or to a randomized siNA control with the same overall length and chemistry, but randomly substituted at each position. Primary and secondary lead reagents are chosen

for the target and optimization performed. After an optimal transfection agent concentration is chosen, a RNA time-course of inhibition is performed with the lead siNA molecule. In addition, a cell-plating format can be used to determine RNA inhibition.

5 Delivery of siNA to Cells

Cells (e.g., COS-1, PC12 or A375 cells) are seeded, for example, at 1×10^5 cells per well of a six-well dish in EGM-2 (BioWhittaker) the day before transfection. siNA (final concentration, for example 20nM) and cationic lipid (e.g., final concentration $2 \mu\text{g/ml}$) are complexed in EGM basal media (Biowhittaker) at 37°C for 30 minutes in polystyrene tubes. Following vortexing, the complexed siNA is added to each well and incubated for the times indicated. For initial optimization experiments, cells are seeded, for example, at 1×10^3 in 96 well plates and siNA complex added as described. Efficiency of delivery of siNA to cells is determined using a fluorescent siNA complexed with lipid. Cells in 6-well dishes are incubated with siNA for 24 hours, rinsed with PBS and fixed in 2% paraformaldehyde for 15 minutes at room temperature. Uptake of siNA is visualized using a fluorescent microscope.

Taqman and Lightcycler quantification of mRNA

Total RNA is prepared from cells following siNA delivery, for example, using Qiagen RNA purification kits for 6-well or Rneasy extraction kits for 96-well assays. For Taqman analysis, dual-labeled probes are synthesized with the reporter dye, FAM or JOE, covalently linked at the 5'-end and the quencher dye TAMRA conjugated to the 3'-end. One-step RT-PCR amplifications are performed on, for example, an ABI PRISM 7700 Sequence Detector using 50 μl reactions consisting of 10 μl total RNA, 100 nM forward primer, 900 nM reverse primer, 100 nM probe, 1X TaqMan PCR reaction buffer (PE-Applied Biosystems), 5.5 mM MgCl_2 , 300 μM each dATP, dCTP, dGTP, and dTTP, 10U RNase Inhibitor (Promega), 1.25U AmpliTaq Gold (PE-Applied Biosystems) and 10U M-MLV Reverse Transcriptase (Promega). The thermal cycling conditions can consist of 30 minutes at 48°C , 10 minutes at 95°C , followed by 40 cycles of 15 seconds at 95°C and 1 minute at 60°C . Quantitation of mRNA levels is determined relative to standards generated from serially diluted total cellular RNA (300, 100, 33, 11 ng/rxn)

and normalizing to β -actin or GAPDH mRNA in parallel TaqMan reactions. For each gene of interest an upper and lower primer and a fluorescently labeled probe are designed. Real time incorporation of SYBR Green I dye into a specific PCR product can be measured in glass capillary tubes using a lightcycler. A standard curve is generated for each primer pair using control cRNA. Values are represented as relative expression to GAPDH in each sample.

Western blotting

Nuclear extracts can be prepared using a standard micro preparation technique (see for example Andrews and Faller, 1991, *Nucleic Acids Research*, 19, 2499). Protein extracts from supernatants are prepared, for example using TCA precipitation. An equal volume of 20% TCA is added to the cell supernatant, incubated on ice for 1 hour and pelleted by centrifugation for 5 minutes. Pellets are washed in acetone, dried and resuspended in water. Cellular protein extracts are run on a 10% Bis-Tris NuPage (nuclear extracts) or 4-12% Tris-Glycine (supernatant extracts) polyacrylamide gel and transferred onto nitro-cellulose membranes. Non-specific binding can be blocked by incubation, for example, with 5% non-fat milk for 1 hour followed by primary antibody for 16 hour at 4°C. Following washes, the secondary antibody is applied, for example (1:10,000 dilution) for 1 hour at room temperature and the signal detected with SuperSignal reagent (Pierce).

Other Assays

Other useful assays in evaluating siNA molecules of the invention are described in Davidson *et al.*, WO 04/013280.

Example 8: Animal Models useful to evaluate the down-regulation of HD gene expression

Evaluating the efficacy of anti-HD agents in animal models is an important prerequisite to human clinical trials. Although the HD mRNA and protein product (huntingtin) show widespread distribution, the progressive neurodegeneration is selective in location, with regional neuron loss and gliosis in striatum, cerebral cortex, thalamus, subthalamus, and hippocampus. An experimental transgenic mouse model has utilized

widespread expression of full-length human HD cDNA in mice with either 16, 48, or 89 CAG repeats. Only mice with 48 or 89 CAG repeats manifested progressive behavioral and motor dysfunction with neuron loss and gliosis in striatum, cerebral cortex, thalamus, and hippocampus (Reddy *et al.*, 1998, *Nature Genet.* 20, 198-202). These animals represent a clinically relevant model for HD pathogenesis and can provide insight into the underlying pathophysiologic mechanisms of other triplet repeat disorders. Other neurodegenerative animal models as are known in the art can similarly be utilized to evaluate siNA molecules of the invention, for example models that utilize systemic or localized delivery (e.g., direct injection, intrathecal delivery, osmotic pump etc.) of therapeutic compounds to the CNS, (see for example Ryu *et al.*, 2003, *Exp Neurol.*, 183, 700-4). As such, this model provides an animal model for testing therapeutic drugs, including siNA constructs of the instant invention.

Example 9: RNAi mediated inhibition of HD expression in cell culture

Inhibition of HD RNA expression using siNA targeting HD RNA

siNA constructs (**Table III**) are tested for efficacy in reducing HD RNA expression in, for example, COS-1 cells. Cells are plated approximately 24 hours before transfection in 96-well plates at 5,000-7,500 cells/well, 100 μ l/well, such that at the time of transfection cells are 70-90% confluent. For transfection, annealed siNAs are mixed with the transfection reagent (Lipofectamine 2000, Invitrogen) in a volume of 50 μ l/well and incubated for 20 min. at room temperature. The siNA transfection mixtures are added to cells to give a final siNA concentration of 25 nM in a volume of 150 μ l. Each siNA transfection mixture is added to 3 wells for triplicate siNA treatments. Cells are incubated at 37° for 24h in the continued presence of the siNA transfection mixture. At 24h, RNA is prepared from each well of treated cells. The supernatants with the transfection mixtures are first removed and discarded, then the cells are lysed and RNA prepared from each well. Target gene expression following treatment is evaluated by RT-PCR for the target gene and for a control gene (36B4, an RNA polymerase subunit) for normalization. The triplicate data is averaged and the standard deviations determined for each treatment. Normalized data are graphed and the percent reduction of target mRNA by active siNAs in comparison to their respective inverted control siNAs is determined.

In a non-limiting example, siNA molecules targeting human huntingtin (HD) were evaluated in cell culture using the transgenic allele (HD82Q) used to make the HD model N171-82Q. A myc tag to the HD protein was utilized for western blot analysis. HEK-293 cells were transfected with HD82Q-myc construct alone or with active siNA constructs 1, 2, and 3 (Sirna Compound Nos. 31993/31994, 31995/31996, 31997/31998 respectively, Table III) or matched chemistry inverted control constructs 4, 5, and 6 (Sirna Compound Nos. 31999/32000, 32001/32002, 32003/32004 respectively, Table III) at two concentrations (0.5 ng and 5 ng) using lipofectamine 2000. Cells were harvested 48 hours later and protein extracts run on SDS-PAGE, blotted to nitrocellulose, and probed with anti-myc antibodies. Neomycin phosphotransferase is expressed on the same plasmid as the myc-tagged construct, allowing for a transfection control. The experiment was run in duplicate. As shown in **Figure 22**, the active siNA constructs (Sirna Compound Nos. 31993/31994, 31995/31996, 31997/31998) all demonstrate inhibition of HD82Q-myc compared with the inverted matched chemistry siNA constructs. Furthermore, the active siNA constructs show selectivity for inhibiting the myc tagged HD82Q compared to c-myc and the neomycin transfection control. Additional experiments are utilized to evaluate silencing of the full-length HD construct by western blot and QPCR. This rapid in vitro screen is useful for identifying effective siNA constructs prior to in vivo studies, utilizing for example N171-82Q mice.

20 Example 10: Indications

The present body of knowledge in HD research indicates the need for methods to assay HD activity and for compounds that can regulate HD expression for research, diagnostic, and therapeutic use. As described herein, the nucleic acid molecules of the present invention can be used in assays to diagnose disease state related of HD levels. In addition, the nucleic acid molecules can be used to treat disease state related to HD levels.

Particular conditions and disease states that can be associated with HD expression modulation include, but are not limited to Huntington disease and related conditions such as progressive chorea, rigidity, dementia, and seizures, spinocerebellar ataxia, spinal and bulbar muscular dystrophy (SBMA), dentatorubropallidoluysian atrophy (DRPLA), and any other diseases or conditions that are related to or will respond to the levels of a

repeat expansion (RE) protein in a cell or tissue, alone or in combination with other therapies.

The use of caspase inhibitors, agents that disrupt RE protein aggregation, and neuroprotective agents (e.g., pyridoxine) are non-limiting examples of chemotherapeutic agents that can be combined with or used in conjunction with the nucleic acid molecules (e.g. siNA molecules) of the instant invention. Those skilled in the art will recognize that other anti-cancer compounds and therapies can similarly be readily combined with the nucleic acid molecules of the instant invention (e.g. siNA molecules) and are hence within the scope of the instant invention.

10 Example 11: Diagnostic uses

The siNA molecules of the invention can be used in a variety of diagnostic applications, such as in the identification of molecular targets (e.g., RNA) in a variety of applications, for example, in clinical, industrial, environmental, agricultural and/or research settings. Such diagnostic use of siNA molecules involves utilizing reconstituted RNAi systems, for example, using cellular lysates or partially purified cellular lysates. siNA molecules of this invention can be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of endogenous or exogenous, for example viral, RNA in a cell. The close relationship between siNA activity and the structure of the target RNA allows the detection of mutations in any region of the molecule, which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple siNA molecules described in this invention, one can map nucleotide changes, which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with siNA molecules can be used to inhibit gene expression and define the role of specified gene products in the progression of disease or infection. In this manner, other genetic targets can be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple siNA molecules targeted to different genes, siNA molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations siNA molecules and/or other chemical or biological molecules). Other *in vitro* uses of siNA molecules of this invention are well known in the art, and include detection of the

presence of mRNAs associated with a disease, infection, or related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with a siNA using standard methodologies, for example, fluorescence resonance emission transfer (FRET).

5 In a specific example, siNA molecules that cleave only wild-type or mutant forms of the target RNA are used for the assay. The first siNA molecules (*i.e.*, those that cleave only wild-type forms of target RNA) are used to identify wild-type RNA present in the sample and the second siNA molecules (*i.e.*, those that cleave only mutant forms of target RNA) are used to identify mutant RNA in the sample. As reaction controls,
10 synthetic substrates of both wild-type and mutant RNA are cleaved by both siNA molecules to demonstrate the relative siNA efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus, each analysis requires two siNA
15 molecules, two substrates and one unknown sample, which is combined into six reactions. The presence of cleavage products is determined using an RNase protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic
20 changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (*i.e.*, disease related or infection related) is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels is adequate and decreases the cost of the initial diagnosis. Higher mutant form to wild-type ratios are correlated with higher risk
25 whether RNA levels are compared qualitatively or quantitatively.

 All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

30 One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as

those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are
5 defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications can be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims. The present invention teaches
10 one skilled in the art to test various combinations and/or substitutions of chemical modifications described herein toward generating nucleic acid constructs with improved activity for mediating RNAi activity. Such improved activity can comprise improved stability, improved bioavailability, and/or improved activation of cellular responses mediating RNAi. Therefore, the specific embodiments described herein are not limiting
15 and one skilled in the art can readily appreciate that specific combinations of the modifications described herein can be tested without undue experimentation toward identifying siNA molecules with improved RNAi activity.

The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically
20 disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and
25 described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be
30 within the scope of this invention as defined by the description and the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

Table I: POLYQ repeat Accession Numbers

5	NM_002111 Homo sapiens huntingtin (Huntington disease) (HD), mRNA gi 38788404 ref NM_002111.4 [38788404]
10	AB016794 Homo sapiens mRNA for huntingtin, complete cds gi 4126798 dbj AB016794.1 [4126798]
15	L12392 Homo sapiens Huntington's Disease (HD) mRNA, complete cds gi 1709991 gb L12392.1 HUMHDA[1709991]
20	AC005516 Homo sapiens Chromosome 4p16.3 BAC clone 399e10 containing Huntington's Disease gene; exons 1-67, complete sequence gi 3900835 gb AC005516.1 AC005516[3900835]
25	AL390059 Human DNA sequence from clone RP11-399E10 on chromosome 4, complete sequence
30	gi 26984367 emb AL390059.9 [26984367]
	Z69837 Human DNA sequence from clone LA04NC01-113B6 on chromosome 4, complete sequence
35	gi 1212949 emb Z69837.1 HSL113B6[1212949]
	L20431 Homo sapiens Huntington disease-associated protein (HD) mRNA, complete cds
40	gi 398028 gb L20431.1 HUMHUNTDIS[398028]
45	NM_000332 Homo sapiens spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1) (SCA1), mRNA gi 4506792 ref NM_000332.1 [4506792]

- X79204
H.sapiens SCA1 mRNA for ataxin
5 gi|529661|emb|X79204.1|HSSCA1[529661]
- AL009031
Human DNA sequence from clone RP3-467D16 on chromosome
10 6p22.3-24.1 Contains the
5' end of the SCA1 gene for spinocerebellar ataxia 1
(olivopontocerebellar
ataxia 1, autosomal dominant, ataxin 1) with a poly-
glutamine (CAG repeat)
15 polymorphism and the 3' part of the GMPR gene for GMP
reductase, Guanosine
5'-monophosphate oxidoreductase, complete sequence
gi|2808422|emb|AL009031.1|HS467D16[2808422]
- 20 S64648
SCA1 {CAG repeat} [human, Genomic Mutant, 506 nt]
gi|407593|bbm|316393|bbs|136468|gb|S64648.1|S64648[407593]
- 25 BC047894
Homo sapiens spinocerebellar ataxia 1 (olivopontocerebellar
ataxia 1, autosomal
dominant, ataxin 1), mRNA (cDNA clone IMAGE:4472404),
30 partial cds
gi|28839052|gb|BC047894.1|[28839052]
- NM_002973
35 Homo sapiens spinocerebellar ataxia 2 (olivopontocerebellar
ataxia 2, autosomal
dominant, ataxin 2) (SCA2), mRNA
gi|4506794|ref|NM_002973.1|[4506794]
- 40 U70323
Human ataxin-2 (SCA2) mRNA, complete cds
gi|1679683|gb|U70323.1|HSU70323[1679683]
- 45 Y08262
H.sapiens mRNA for SCA2 protein
gi|1770389|emb|Y08262.1|HSDANSCA2[1770389]

- AK095017
Homo sapiens cDNA FLJ37698 fis, clone BRHIP2015679, highly similar to Human
5 ataxin-2 (SCA2) mRNA
gi|21754198|dbj|AK095017.1|[21754198]
- BC033711
10 Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3), mRNA (cDNA clone MGC:44934 IMAGE:4393766), complete cds
15 gi|21708051|gb|BC033711.1|[21708051]
- U64822
Homo sapiens josephin MJD1 mRNA, partial cds
20 gi|2262198|gb|U64822.1|HSU64822[2262198]
- S75313
MJD1=MJD1 protein {CAG repeats} [human, brain, mRNA, 1776 nt]
25 gi|833927|bbm|360325|bbs|160590|gb|S75313.1|S75313[833927]
- NM_004993
30 Homo sapiens Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3) (MJD), transcript variant 1, mRNA
35 gi|13518018|ref|NM_004993.2|[13518018]
- U64821
Homo sapiens josephin MJD1 mRNA, cds
40 gi|2262196|gb|U64821.1|HSU64821[2262196]
- U64820
Homo sapiens josephin MJD1 mRNA, complete cds
45 gi|2262194|gb|U64820.1|HSU64820[2262194]
- AB050194
Homo sapiens mRNA for ataxin-3, complete cds

gi|11559485|dbj|AB050194.1|[11559485]

NM_030660
 5 Homo sapiens Machado-Joseph disease (spinocerebellar ataxia
 3,
 olivopontocerebellar ataxia 3, autosomal dominant, ataxin
 3) (MJD), transcript
 variant 2, mRNA
 10 gi|13518012|ref|NM_030660.1|[13518012]

BC022245
 15 Homo sapiens Machado-Joseph disease (spinocerebellar ataxia
 3,
 olivopontocerebellar ataxia 3, autosomal dominant, ataxin
 3), mRNA (cDNA clone
 IMAGE:4717161), containing frame-shift errors
 gi|18490814|gb|BC022245.1|[18490814]
 20

AB038653
 Homo sapiens genomic DNA, chromosome 14q32.1, BAC
 clone:B445M7
 25 gi|14149091|dbj|AB038653.1|[14149091]

AJ000501
 Homo sapiens DNA for CAG/CTG repeat region
 30 gi|2274960|emb|AJ000501.1|HSCAGCTG[2274960]

NM_000068
 35 Homo sapiens calcium channel, voltage-dependent, P/Q type,
 alpha 1A subunit
 (CACNA1A), transcript variant 1, mRNA
 gi|13386499|ref|NM_000068.2|[13386499]

40 NM_023035
 Homo sapiens calcium channel, voltage-dependent, P/Q type,
 alpha 1A subunit
 (CACNA1A), transcript variant 2, mRNA
 gi|13386497|ref|NM_023035.1|[13386497]
 45

U79666
 Homo sapiens alpha1A-voltage-dependent calcium channel
 mRNA, splice form

- BI-1-Vi-GGCAG, complete cds
gi|2281751|gb|U79666.1|HSU79666[2281751]
- 5 X99897
H.sapiens mRNA for P/Q-type calcium channel alpha1 subunit
gi|1657332|emb|X99897.1|HSPQCCA1[1657332]
- 10 AB035726
Homo sapiens CACNA1A mRNA for alpha1A-voltage-dependent
calcium channel, partial
cds, isolate:TMDN-SCA6-001
gi|7630180|dbj|AB035726.1|[7630180]
- 15
AF004883
Homo sapiens neuronal calcium channel alpha 1A subunit
isoform 1A-2 mRNA,
complete cds
20 gi|2213910|gb|AF004883.1|AF004883[2213910]
- AF004884
25 Homo sapiens neuronal calcium channel alpha 1A subunit
isoform A-1 mRNA,
complete cds
gi|2213912|gb|AF004884.1|AF004884[2213912]
- 30
AB035727
Homo sapiens CACNA1A mRNA for alpha1A-voltage-dependent
calcium channel,
complete cds, isolate:TMDN-CNT-001
35 gi|9711928|dbj|AB035727.2|[9711928]
- U06702
40 Human clone CCA54 mRNA containing CCA trinucleotide repeat
gi|476266|gb|U06702.1|HSU06702[476266]
- NM_000333
45 Homo sapiens spinocerebellar ataxia 7 (olivopontocerebellar
atrophy with retinal
degeneration) (SCA7), mRNA
gi|4506796|ref|NM_000333.1|[4506796]

AJ000517
Homo Sapiens mRNA for spinocerebellar ataxia 7
gi|2370154|emb|AJ000517.1|HSSCA7[2370154]

5
AF032105
Homo sapiens ataxin-7 (SCA7) mRNA, complete cds
gi|3192953|gb|AF032105.1|AF032105[3192953]

10
AF032103
Homo sapiens ataxin-7 (SCA7) mRNA, 3' end, partial cds
gi|3192949|gb|AF032103.1|AF032103[3192949]

15
AK125125
Homo sapiens cDNA FLJ43135 fis, clone CTONG3006629
gi|34531113|dbj|AK125125.1|[34531113]

20
AF020275
Homo sapiens expanded SCA7 CAG repeat
gi|2501955|gb|AF020275.1|AF020275[2501955]

25
NM_004576
Homo sapiens protein phosphatase 2 (formerly 2A),
regulatory subunit B (PR 52),
beta isoform (PPP2R2B), transcript variant 1, mRNA
30 gi|32307122|ref|NM_004576.2|[32307122]

M64930
Human protein phosphatase 2A beta subunit mRNA, complete
35 cds
gi|190423|gb|M64930.1|HUMPROP2AB[190423]

NM_181675
40 Homo sapiens protein phosphatase 2 (formerly 2A),
regulatory subunit B (PR 52),
beta isoform (PPP2R2B), transcript variant 3, mRNA
gi|32307114|ref|NM_181675.1|[32307114]

45
NM_181674
Homo sapiens protein phosphatase 2 (formerly 2A),
regulatory subunit B (PR 52),
beta isoform (PPP2R2B), transcript variant 2, mRNA

gi|32307112|ref|NM_181674.1|[32307112]

BC031790

- 5 Homo sapiens protein phosphatase 2 (formerly 2A),
regulatory subunit B (PR 52),
beta isoform, transcript variant 2, mRNA (cDNA clone
MGC:24888 IMAGE:4939981),
complete cds
10 gi|21619304|gb|BC031790.1|[21619304]

AK056192

- 15 Homo sapiens cDNA FLJ31630 fis, clone NT2RI2003361, highly
similar to PROTEIN
PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, NEURONAL
ISOFORM
gi|16551529|dbj|AK056192.1|[16551529]

20

NM_000044

- Homo sapiens androgen receptor (dihydrotestosterone
receptor; testicular
feminization; spinal and bulbar muscular atrophy; Kennedy
25 disease) (AR), mRNA
gi|21322251|ref|NM_000044.2|[21322251]

M20132

- 30 Human androgen receptor (AR) mRNA, complete cds
gi|178627|gb|M20132.1|HUMANREC[178627]

M21748

- 35 Human androgen receptor mRNA, complete cds, clones A1 and
J8
gi|178871|gb|M21748.1|HUMARA[178871]

40 M73069

Human androgen receptor mutant gene, mRNA, complete cds
gi|178655|gb|M73069.1|HUMANRE[178655]

45 BC051795

Homo sapiens dentatorubral-pallidoluysian atrophy
(atrophin-1), mRNA (cDNA clone
MGC:57647 IMAGE:4181592), complete cds
gi|34193087|gb|BC051795.2|[34193087]

- NM_001940
Homo sapiens dentatorubral-pallidoluysian atrophy
5 (atrophin-1) (DRPLA), mRNA
gi|6005998|ref|NM_001940.2|[6005998]
- U23851
10 Human atrophin-1 mRNA, complete cds
gi|915325|gb|U23851.1|HSU23851[915325]
- D38529
15 Homo sapiens mRNA for DRPLA protein, complete cds
gi|1732443|dbj|D38529.1|HUMDRPLA[1732443]
- D31840
20 Homo sapiens DRPLA mRNA, complete cds
gi|862329|dbj|D31840.1|HUMDRPLA1[862329]
- AC006512
25 Homo sapiens 12 PAC RP3-461F17 (Roswell Park Cancer
Institute Human PAC Library)
complete sequence
gi|29469488|gb|AC006512.13|[29469488]
- 30

Table II: HD siNA and Target Sequences

dbSNP ID	Pos	Target Seq	Seq ID	UPos	Upper seq	SeqID	LPos	Lower seq	Seq ID
rs396875	85	CAAUCAUGCUGGCCGGCGG	1	85	CAAUCAUGCUGGCCGGCGG	1	103	ACGCCGGCCAGCAUGAUU	1753
rs396875	86	AUCAUGCUGGCCGGCGG	2	86	AUCAUGCUGGCCGGCGG	2	104	CACGCCGGCCAGCAUGAU	1754
rs396875	87	AUCAUGCUGGCCGGCGG	3	87	AUCAUGCUGGCCGGCGG	3	105	CCACGCCGGCCAGCAUGAU	1755
rs396875	88	UCAUGCUGGCCGGCGG	4	88	AUCAUGCUGGCCGGCGG	4	106	GCCACGCCGGCCAGCAUGA	1756
rs396875	89	CAUGCUGGCCGGCGG	5	89	CAUGCUGGCCGGCGG	5	107	GGCCACGCCGGCCAGCAUG	1757
rs396875	90	AUGCUGGCCGGCGG	6	90	AUGCUGGCCGGCGG	6	108	GGCCACGCCGGCCAGCAU	1758
rs396875	91	UGCUGGCCGGCGG	7	91	UGCUGGCCGGCGG	7	109	GGGCCACGCCGGCCAGCA	1759
rs396875	92	GCUGGCCGGCGG	8	92	GCUGGCCGGCGG	8	110	CGGGCCACGCCGGCCAGC	1760
rs396875	93	CUGGCCGGCGG	9	93	CUGGCCGGCGG	9	111	GCGGGCCACGCCGGCCAG	1761
rs396875	94	UGGCCGGCGG	10	94	UGGCCGGCGG	10	112	GGCGGGCCACGCCGGCCA	1762
rs396875	95	GGCGGGCGG	11	95	GGCGGGCGG	11	113	AGCGGGCCACGCCGGCC	1763
rs396875	96	GCGGGCGG	12	96	GCGGGCGG	12	114	GAGCGGGCCACGCCGGCC	1764
rs396875	97	CCGGCGG	13	97	CCGGCGG	13	115	GGAGCGGGCCACGCCGG	1765
rs396875	98	CGCGG	14	98	CGCGG	14	116	CGAGCGGGCCACGCCGG	1766
rs396875	99	GGCGG	15	99	GGCGG	15	117	GCGAGCGGGCCACGCC	1767
rs396875	100	GCGUGGCCCGCCUCCGC	16	100	GCGUGGCCCGCCUCCGC	16	118	GGCGAGCGGGCCACGCC	1768
rs396875	101	CGUGGCCCGCCUCCGC	17	101	CGUGGCCCGCCUCCGC	17	119	CGCGGAGCGGGCCACGCC	1769
rs396875	102	GUGGCCCGCCUCCGC	18	102	GUGGCCCGCCUCCGC	18	120	CCGCGGAGCGGGCCAC	1770
rs396875	103	UGGCCCGCCUCCGC	19	103	UGGCCCGCCUCCGC	19	121	GCGCGGAGCGGGCCCA	1771
rs396875	85	CAAUCAUGCUGGCCGGCGG	20	85	CAAUCAUGCUGGCCGGCGG	20	103	GCGCGGGCCAGCAUGAU	1772
rs396875	86	AUCAUGCUGGCCGGCGG	21	86	AUCAUGCUGGCCGGCGG	21	104	CGCGCGGGCCAGCAUGAU	1773
rs396875	87	AUCAUGCUGGCCGGCGG	22	87	AUCAUGCUGGCCGGCGG	22	105	CCGCGCGGGCCAGCAUGA	1774
rs396875	88	UCAUGCUGGCCGGCGG	23	88	UCAUGCUGGCCGGCGG	23	106	GCCGCGGGCCAGCAUGA	1775
rs396875	89	CAUGCUGGCCGGCGG	24	89	CAUGCUGGCCGGCGG	24	107	GGCGCGGGCCAGCAUG	1776
rs396875	90	AUGCUGGCCGGCGG	25	90	AUGCUGGCCGGCGG	25	108	GGCGCGGGCCAGCAU	1777
rs396875	91	UGCUGGCCGGCGG	26	91	UGCUGGCCGGCGG	26	109	GGGCGCGGGCCAGCA	1778
rs396875	92	GCUGGCCGGCGG	27	92	GCUGGCCGGCGG	27	110	GCGGCGCGGGCCAGC	1779
rs396875	93	CUGGCCGGCGG	28	93	CUGGCCGGCGG	28	111	GCGGGCGGGCCAGC	1780
rs396875	94	UGGCCGGCGG	29	94	UGGCCGGCGG	29	112	GGCGGGCGGGCCAGCA	1781
rs396875	95	GGCGGGCGG	30	95	GGCGGGCGG	30	113	AGCGGGCGGGCCAGC	1782
rs396875	96	GCGGGCGG	31	96	GCGGGCGG	31	114	GAGCGGGCGGGCCAGC	1783
rs396875	97	CCGGCGG	32	97	CCGGCGG	32	115	GGAGCGGGCGGGCCAGC	1784
rs396875	98	CGCGCGG	33	98	CGCGCGG	33	116	GCGAGCGGGCGGGCCAGC	1785
rs396875	99	GGCGCGG	34	99	GGCGCGG	34	117	GCGAGCGGGCGGGCCAGC	1786
rs396875	100	GCGCGGCCCGCCUCCGC	35	100	GCGCGGCCCGCCUCCGC	35	118	GCGGAGCGGGCGGGCCAGC	1787

rs396875	101	CGGGCCCCCGCCUCCGCG	36	101	CGGGCCCCCGCCUCCGCG	36	119	CGGGGAGGGGGGCGCG	1788
rs396875	102	CGGGCCCCCGCCUCCGCGG	37	102	CGGGCCCCCGCCUCCGCGG	37	120	CGGGCGAGGGGGGCGCG	1789
rs396875	103	CGGGCCCCCGCCUCCGCGG	38	103	CGGGCCCCCGCCUCCGCGG	38	121	GGGGGGAGGGGGGCGCG	1790
rs10701858	328	GAAAGCUGAUGAAGGCCU	39	328	GAAAGCUGAUGAAGGCCU	39	346	AGGCCUUAUCAGCUUUU	1791
rs10701858	329	AAAAGCUGAUGAAGGCCU	40	329	AAAAGCUGAUGAAGGCCU	40	347	AAGCCUUAUCAGCUUUU	1792
rs10701858	330	AAAGCUGAUGAAGGCCUUC	41	330	AAAGCUGAUGAAGGCCUUC	41	348	GAAGGCCUUAUCAGCUU	1793
rs10701858	331	AAGCUGAUGAAGGCCUUCG	42	331	AAGCUGAUGAAGGCCUUCG	42	349	CGAAGGCCUUAUCAGCU	1794
rs10701858	332	AGCUGAUGAAGGCCUUCGA	43	332	AGCUGAUGAAGGCCUUCGA	43	350	UCGAAGGCCUUAUCAGCU	1795
rs10701858	333	GCUGAUGAAGGCCUUCGAG	44	333	GCUGAUGAAGGCCUUCGAG	44	351	CUCGAAGGCCUUAUCAGC	1796
rs10701858	334	CUGAUGAAGGCCUUCGAGU	45	334	CUGAUGAAGGCCUUCGAGU	45	352	ACUCGAAGGCCUUAUCAG	1797
rs10701858	335	UGAUGAAGGCCUUCGAGUC	46	335	UGAUGAAGGCCUUCGAGUC	46	353	GACUCGAAGGCCUUAUCA	1798
rs10701858	336	GAUGAAGGCCUUCGAGUCC	47	336	GAUGAAGGCCUUCGAGUCC	47	354	GGACUCGAAGGCCUUAUC	1799
rs10701858	337	AUGAAGGCCUUCGAGUCCC	48	337	AUGAAGGCCUUCGAGUCCC	48	355	GGGACUCGAAGGCCUUAU	1800
rs10701858	338	UGAAGGCCUUCGAGUCCCU	49	338	UGAAGGCCUUCGAGUCCCU	49	356	AGGACUCGAAGGCCUUA	1801
rs10701858	339	GAAGGCCUUCGAGUCCUC	50	339	GAAGGCCUUCGAGUCCUC	50	357	GAGGACUCGAAGGCCUUC	1802
rs10701858	340	AAGGCCUUCGAGUCCUCA	51	340	AAGGCCUUCGAGUCCUCA	51	358	UGAGGACUCGAAGGCCUU	1803
rs10701858	341	AGGCCUUCGAGUCCUCA	52	341	AGGCCUUCGAGUCCUCA	52	359	UUGAGGACUCGAAGGCCU	1804
rs10701858	342	GGCCUUCGAGUCCUCAAG	53	342	GGCCUUCGAGUCCUCAAG	53	360	CUUGAGGACUCGAAGGCC	1805
rs10701858	343	GCCUUCGAGUCCUCAAGU	54	343	GCCUUCGAGUCCUCAAGU	54	361	ACUUGAGGACUCGAAGGC	1806
rs10701858	344	CCUUCGAGUCCUCAAGU	55	344	CCUUCGAGUCCUCAAGU	55	362	ACUUGAGGACUCGAAGG	1807
rs10701858	328	GAAAGCUGAUGAAGGCCG	56	328	GAAAGCUGAUGAAGGCCG	56	346	CGGCCUUAUCAGCUUUU	1808
rs10701858	329	AAAAGCUGAUGAAGGCCG	57	329	AAAAGCUGAUGAAGGCCG	57	347	CGGCCUUAUCAGCUUUU	1809
rs10701858	330	AAAGCUGAUGAAGGCCGCC	58	330	AAAGCUGAUGAAGGCCGCC	58	348	GGCGGCCUUAUCAGCUU	1810
rs10701858	331	AAGCUGAUGAAGGCCGCCU	59	331	AAGCUGAUGAAGGCCGCCU	59	349	AGCGGCCUUAUCAGCUU	1811
rs10701858	332	AGCUGAUGAAGGCCGCCUU	60	332	AGCUGAUGAAGGCCGCCUU	60	350	AAGCGGCCUUAUCAGCU	1812
rs10701858	333	GCUGAUGAAGGCCGCCUUC	61	333	GCUGAUGAAGGCCGCCUUC	61	351	GAAGCGGCCUUAUCAGC	1813
rs10701858	334	CUGAUGAAGGCCGCCUUCG	62	334	CUGAUGAAGGCCGCCUUCG	62	352	CGAAGCGGCCUUAUCAG	1814
rs10701858	335	UGAUGAAGGCCGCCUUCGA	63	335	UGAUGAAGGCCGCCUUCGA	63	353	UCGAAGCGGCCUUAUCA	1815
rs10701858	336	GAUGAAGGCCGCCUUCGAG	64	336	GAUGAAGGCCGCCUUCGAG	64	354	CUCGAAGCGGCCUUAUC	1816
rs10701858	337	AUGAAGGCCGCCUUCGAGU	65	337	AUGAAGGCCGCCUUCGAGU	65	355	ACUCGAAGCGGCCUUAU	1817
rs10701858	338	UGAAGGCCGCCUUCGAGUC	66	338	UGAAGGCCGCCUUCGAGUC	66	356	GACUCGAAGCGGCCUUA	1818
rs10701858	339	GAAGGCCGCCUUCGAGUCC	67	339	GAAGGCCGCCUUCGAGUCC	67	357	GGACUCGAAGCGGCCUUC	1819
rs10701858	340	AAGGCCGCCUUCGAGUCCC	68	340	AAGGCCGCCUUCGAGUCCC	68	358	GGGACUCGAAGCGGCCUU	1820
rs10701858	341	AGGCCGCCUUCGAGUCCCU	69	341	AGGCCGCCUUCGAGUCCCU	69	359	AGGGACUCGAAGCGGCCU	1821
rs10701858	342	GGCCGCCUUCGAGUCCCU	70	342	GGCCGCCUUCGAGUCCCU	70	360	GAGGACUCGAAGCGGCC	1822
rs10701858	343	GCCGCCUUCGAGUCCCUA	71	343	GCCGCCUUCGAGUCCCUA	71	361	UGAGGACUCGAAGCGGCG	1823
rs10701858	344	CGCCUUCGAGUCCCUCAA	72	344	CGCCUUCGAGUCCCUCAA	72	362	UUGAGGACUCGAAGCGG	1824
rs10701858	345	CGCCUUCGAGUCCCUCAAG	73	345	CGCCUUCGAGUCCCUCAAG	73	363	CUUGAGGACUCGAAGGCG	1825
rs1936033	1070	UUUUGUUAAAGGCCUUAU	74	1070	UUUUGUUAAAGGCCUUAU	74	1088	AUGAAGGCCUUAACAAAA	1826

rs1936033	1071	UUUGUUAAAGGCCUUCAUA	75	1071	UUUGUUAAAGGCCUUCAUA	75	1089	UAUGAAGGCCUUUAACAA	1827
rs1936033	1072	UUUGUUAAAGGCCUUCAUAG	76	1072	UUUGUUAAAGGCCUUCAUAG	76	1090	CUAUGAAGGCCUUUAACAA	1828
rs1936033	1073	UGUUAAAGGCCUUCAUAGC	77	1073	UGUUAAAGGCCUUCAUAGC	77	1091	GCUAUGAAGGCCUUUAACA	1829
rs1936033	1074	GUUAAAGGCCUUCAUAGCG	78	1074	GUUAAAGGCCUUCAUAGCG	78	1092	CGCUAUGAAGGCCUUUAAC	1830
rs1936033	1075	UUAAGGCCUUCAUAGCGA	79	1075	UUAAGGCCUUCAUAGCGA	79	1093	UCGCUAUGAAGGCCUUUA	1831
rs1936033	1076	UAAAGGCCUUCAUAGCGAA	80	1076	UAAAGGCCUUCAUAGCGAA	80	1094	UUCGCUAUGAAGGCCUUUA	1832
rs1936033	1077	AAAGGCCUUCAUAGCGAAC	81	1077	AAAGGCCUUCAUAGCGAAC	81	1095	GUUCGCUAUGAAGGCCUUU	1833
rs1936033	1078	AAGCCUUCAUAGCGAAC	82	1078	AAGCCUUCAUAGCGAAC	82	1096	GGUUCGCUAUGAAGGCCUU	1834
rs1936033	1079	AGCCUUCAUAGCGAACCU	83	1079	AGCCUUCAUAGCGAACCU	83	1097	AGGUUCGCUAUGAAGGCCU	1835
rs1936033	1080	GGCCUUCAUAGCGAACCCUG	84	1080	GGCCUUCAUAGCGAACCCUG	84	1098	CAGGUUCGCUAUGAAGGCC	1836
rs1936033	1081	GCCUUCAUAGCGAACCCUGA	85	1081	GCCUUCAUAGCGAACCCUGA	85	1099	UCAGGUUCGCUAUGAAGGCC	1837
rs1936033	1082	CCUUCAUAGCGAACCCUGAA	86	1082	CCUUCAUAGCGAACCCUGAA	86	1100	UCAGGUUCGCUAUGAAGG	1838
rs1936033	1083	CUUCAUAGCGAACCCUGAAG	87	1083	CUUCAUAGCGAACCCUGAAG	87	1101	CUUCAGGUUCGCUAUGAAG	1839
rs1936033	1084	UUCAUAGCGAACCCUGAAGU	88	1084	UUCAUAGCGAACCCUGAAGU	88	1102	ACUUCAGGUUCGCUAUGAA	1840
rs1936033	1085	UCAUAGCGAACCCUGAAGUC	89	1085	UCAUAGCGAACCCUGAAGUC	89	1103	GACUUCAGGUUCGCUAUGA	1841
rs1936033	1086	CAUAGCGAACCCUGAAGUCA	90	1086	CAUAGCGAACCCUGAAGUCA	90	1104	UGACUUCAGGUUCGCUAUG	1842
rs1936033	1087	AUAGCGAACCCUGAAGUCA	91	1087	AUAGCGAACCCUGAAGUCA	91	1105	UUGACUUCAGGUUCGCUAU	1843
rs1936033	1088	UAGCGAACCCUGAAGUCAAG	92	1088	UAGCGAACCCUGAAGUCAAG	92	1106	CUUGACUUCAGGUUCGCUA	1844
rs1936033	1070	UUUGUUAAAGGCCUUUCAC	93	1070	UUUGUUAAAGGCCUUUCAC	93	1088	GUGAAGGCCUUUAACAAA	1845
rs1936033	1071	UUUGUUAAAGGCCUUUCACA	94	1071	UUUGUUAAAGGCCUUUCACA	94	1089	UGUGAAGGCCUUUAACAAA	1846
rs1936033	1072	UUGUUAAAGGCCUUUCACAG	95	1072	UUGUUAAAGGCCUUUCACAG	95	1090	CUGUGAAGGCCUUUAACAA	1847
rs1936033	1073	UGUUAAAGGCCUUUCACAGC	96	1073	UGUUAAAGGCCUUUCACAGC	96	1091	GCUGUGAAGGCCUUUAACA	1848
rs1936033	1074	GUUAAAGGCCUUUCACAGCG	97	1074	GUUAAAGGCCUUUCACAGCG	97	1092	CGCUGUGAAGGCCUUUAAC	1849
rs1936033	1075	UUAAGGCCUUUCACAGCGA	98	1075	UUAAGGCCUUUCACAGCGA	98	1093	UCGCUGUGAAGGCCUUUA	1850
rs1936033	1076	UAAAGGCCUUUCACAGCGAA	99	1076	UAAAGGCCUUUCACAGCGAA	99	1094	UUCGCUGUGAAGGCCUUUA	1851
rs1936033	1077	AAAGGCCUUUCACAGCGAAC	100	1077	AAAGGCCUUUCACAGCGAAC	100	1095	GUUCGCUGUGAAGGCCUUU	1852
rs1936033	1078	AAGCCUUCACAGCGAAC	101	1078	AAGCCUUCACAGCGAAC	101	1096	GGUUCGCUGUGAAGGCCUU	1853
rs1936033	1079	AGCCUUCACAGCGAACCCU	102	1079	AGCCUUCACAGCGAACCCU	102	1097	AGGUUCGCUGUGAAGGCCU	1854
rs1936033	1080	GGCCUUCACAGCGAACCCUG	103	1080	GGCCUUCACAGCGAACCCUG	103	1098	CAGGUUCGCUGUGAAGGCC	1855
rs1936033	1081	GCCUUCACAGCGAACCCUGA	104	1081	GCCUUCACAGCGAACCCUGA	104	1099	UCAGGUUCGCUGUGAAGGCC	1856
rs1936033	1082	CCUUCACAGCGAACCCUGAA	105	1082	CCUUCACAGCGAACCCUGAA	105	1100	UUCAGGUUCGCUGUGAAGG	1857
rs1936033	1083	CUUCACAGCGAACCCUGAAG	106	1083	CUUCACAGCGAACCCUGAAG	106	1101	CUUCAGGUUCGCUGUGAAG	1858
rs1936033	1084	UUCACAGCGAACCCUGAAGU	107	1084	UUCACAGCGAACCCUGAAGU	107	1102	ACUUCAGGUUCGCUGUGAA	1859
rs1936033	1085	UCACAGCGAACCCUGAAGUC	108	1085	UCACAGCGAACCCUGAAGUC	108	1103	GACUUCAGGUUCGCUGUGA	1860
rs1936033	1086	CACAGCGAACCCUGAAGUCA	109	1086	CACAGCGAACCCUGAAGUCA	109	1104	UGACUUCAGGUUCGCUGUG	1861
rs1936033	1087	ACAGCGAACCCUGAAGUCA	110	1087	ACAGCGAACCCUGAAGUCA	110	1105	UUGACUUCAGGUUCGCUGU	1862
rs1936033	1088	CAGCGAACCCUGAAGUCAAG	111	1088	CAGCGAACCCUGAAGUCAAG	111	1106	CUUGACUUCAGGUUCGCUG	1863
rs1936032	1188	UUGGCUACUAAUUGUCUC	112	1188	UUGGCUACUAAUUGUCUC	112	1206	GAGCACAUUAGUAGCCAA	1864
rs1936032	1189	UGGCUACUAAUUGUCUCU	113	1189	UGGCUACUAAUUGUCUCU	113	1207	AGAGCACAUUAGUAGCCA	1865

rs1936032	1190	GGCUACUAAAUGUGCUCUU	114	1190	GGCUACUAAAUGUGCUCUU	114	1208	AAGAGCACAUUUAGUAGCC	1866
rs1936032	1191	GCUACUAAAUGUGCUCUUA	115	1191	GCUACUAAAUGUGCUCUUA	115	1209	UAGAGCACAUUUAGUAGC	1867
rs1936032	1192	CUACUAAAUGUGCUCUUAAG	116	1192	CUACUAAAUGUGCUCUUAAG	116	1210	CUAAGAGCACAUUUAGUAG	1868
rs1936032	1193	UACUAAAUGUGCUCUUAAGG	117	1193	UACUAAAUGUGCUCUUAAGG	117	1211	CCUAAAGAGCACAUUUAGUA	1869
rs1936032	1194	ACUAAAUGUGCUCUUAAGGC	118	1194	ACUAAAUGUGCUCUUAAGGC	118	1212	GCCUAAAGAGCACAUUUAGU	1870
rs1936032	1195	CUAAAUGUGCUCUUAAGGCU	119	1195	CUAAAUGUGCUCUUAAGGCU	119	1213	AGCCUAAAGAGCACAUUUAG	1871
rs1936032	1196	UAAAUGUGCUCUUAAGGCUU	120	1196	UAAAUGUGCUCUUAAGGCUU	120	1214	AAGCCUAAAGAGCACAUUUUA	1872
rs1936032	1197	AAUUGUGCUCUUAAGGCUUA	121	1197	AAUUGUGCUCUUAAGGCUUA	121	1215	UAAAGCCUAAAGAGCACAUUU	1873
rs1936032	1198	AUUGUGCUCUUAAGGCUUAC	122	1198	AUUGUGCUCUUAAGGCUUAC	122	1216	GUAAAGCCUAAAGAGCACAUU	1874
rs1936032	1199	AUGUGCUCUUAAGGCUUACU	123	1199	AUGUGCUCUUAAGGCUUACU	123	1217	AGUAAAGCCUAAAGAGCACAU	1875
rs1936032	1200	UGUGCUCUUAAGGCUUACUC	124	1200	UGUGCUCUUAAGGCUUACUC	124	1218	GAGUAAAGCCUAAAGAGCAC	1876
rs1936032	1201	GUGCUCUUAAGGCUUACUCG	125	1201	GUGCUCUUAAGGCUUACUCG	125	1219	CGAGUAAAGCCUAAAGAGCAC	1877
rs1936032	1202	UGCUCUUAAGGCUUACUCGU	126	1202	UGCUCUUAAGGCUUACUCGU	126	1220	ACGAGUAAAGCCUAAAGAGCA	1878
rs1936032	1203	GCUCUUAAGGCUUACUCGUU	127	1203	GCUCUUAAGGCUUACUCGUU	127	1221	AACGAGUAAAGCCUAAAGAGC	1879
rs1936032	1204	CUCUUAAGGCUUACUCGUUC	128	1204	CUCUUAAGGCUUACUCGUUC	128	1222	GAACGAGUAAAGCCUAAAGAG	1880
rs1936032	1205	UCUUAAGGCUUACUCGUUCC	129	1205	UCUUAAGGCUUACUCGUUCC	129	1223	GGAACGAGUAAAGCCUAAAGA	1881
rs1936032	1206	CUUAGGCUUACUCGUUCCU	130	1206	CUUAGGCUUACUCGUUCCU	130	1224	AGGAACGAGUAAAGCCUAAAG	1882
rs1936032	1188	UUGGCUACUAAAUGUGCUG	131	1188	UUGGCUACUAAAUGUGCUG	131	1206	CAGCACAUUUAGUAGCCAA	1883
rs1936032	1189	UGGCUACUAAAUGUGCUGU	132	1189	UGGCUACUAAAUGUGCUGU	132	1207	ACAGCACAUUUAGUAGCCA	1884
rs1936032	1190	GGCUACUAAAUGUGCUGUUA	133	1190	GGCUACUAAAUGUGCUGUUA	133	1208	AACAGCACAUUUAGUAGGCC	1885
rs1936032	1191	GCUACUAAAUGUGCUGUUA	134	1191	GCUACUAAAUGUGCUGUUA	134	1209	UACAGCACAUUUAGUAGAGC	1886
rs1936032	1192	CUACUAAAUGUGCUGUUAAG	135	1192	CUACUAAAUGUGCUGUUAAG	135	1210	CUAACAGCACAUUUAGUAG	1887
rs1936032	1193	UACUAAAUGUGCUGUUAAGG	136	1193	UACUAAAUGUGCUGUUAAGG	136	1211	CCUAAACAGCACAUUUAGUA	1888
rs1936032	1194	ACUAAAUGUGCUGUUAAGGC	137	1194	ACUAAAUGUGCUGUUAAGGC	137	1212	GCCUAAACAGCACAUUUUAGU	1889
rs1936032	1195	CUAAAUGUGCUGUUAAGGCU	138	1195	CUAAAUGUGCUGUUAAGGCU	138	1213	AGCCUAAACAGCACAUUUUAG	1890
rs1936032	1196	UAAAUGUGCUGUUAAGGCUU	139	1196	UAAAUGUGCUGUUAAGGCUU	139	1214	AAGCCUAAACAGCACAUUUUA	1891
rs1936032	1197	AAUUGUGCUGUUAAGGCUUA	140	1197	AAUUGUGCUGUUAAGGCUUA	140	1215	UAAAGCCUAAACAGCACAUUU	1892
rs1936032	1198	AUUGUGCUGUUAAGGCUUAC	141	1198	AUUGUGCUGUUAAGGCUUAC	141	1216	GUAAAGCCUAAACAGCACAUU	1893
rs1936032	1199	AUGUGCUGUUAAGGCUUACU	142	1199	AUGUGCUGUUAAGGCUUACU	142	1217	AGUAAAGCCUAAACAGCACAU	1894
rs1936032	1200	UGUGCUGUUAAGGCUUACUC	143	1200	UGUGCUGUUAAGGCUUACUC	143	1218	GAGUAAAGCCUAAACAGCAC	1895
rs1936032	1201	GUGCUGUUAAGGCUUACUCG	144	1201	GUGCUGUUAAGGCUUACUCG	144	1219	CGAGUAAAGCCUAAACAGCAC	1896
rs1936032	1202	UGCUGUUAAGGCUUACUCGU	145	1202	UGCUGUUAAGGCUUACUCGU	145	1220	ACGAGUAAAGCCUAAACAGCA	1897
rs1936032	1203	GCUGUUAAGGCUUACUCGUU	146	1203	GCUGUUAAGGCUUACUCGUU	146	1221	AACGAGUAAAGCCUAAACAGC	1898
rs1936032	1204	CUGUUAAGGCUUACUCGUUC	147	1204	CUGUUAAGGCUUACUCGUUC	147	1222	GAACGAGUAAAGCCUAAACAG	1899
rs1936032	1205	UGUUAAGGCUUACUCGUUCC	148	1205	UGUUAAGGCUUACUCGUUCC	148	1223	GGAACGAGUAAAGCCUAAACA	1900
rs1936032	1206	GUUAGGCUUACUCGUUCCU	149	1206	GUUAGGCUUACUCGUUCCU	149	1224	AGGAACGAGUAAAGCCUAAAC	1901
rs1065745	1491	GCUUCUGCAAACCCUGACC	150	1491	GCUUCUGCAAACCCUGACC	150	1509	GGUCAGGGUUUGCAGAAGC	1902
rs1065745	1492	CUUCUGCAAACCCUGACCG	151	1492	CUUCUGCAAACCCUGACCG	151	1510	CGGUCAGGGUUUGCAGAAG	1903
rs1065745	1493	UUCUGCAAACCCUGACCCGC	152	1493	UUCUGCAAACCCUGACCCGC	152	1511	GCGGUCAGGGUUUGCAGAA	1904

rs1065745	1494	UCUGCAAACCCUGACCGCA	153	1494	UCUGCAAACCCUGACCGCA	153	1512	UGCGGUCAGGGUUUGCAGA	1905
rs1065745	1495	CUGCAAACCCUGACCGCAG	154	1495	CUGCAAACCCUGACCGCAG	154	1513	CUGCGGUCAGGGUUUGCAG	1906
rs1065745	1496	UGCAAACCCUGACCGCAGU	155	1496	UGCAAACCCUGACCGCAGU	155	1514	ACUGCGGUCAGGGUUUGCA	1907
rs1065745	1497	GCAAACCCUGACCGCAGUC	156	1497	GCAAACCCUGACCGCAGUC	156	1515	GACUGCGGUCAGGGUUUGC	1908
rs1065745	1498	CAAACCCUGACCGCAGUCG	157	1498	CAAACCCUGACCGCAGUCG	157	1516	CGACUGCGGUCAGGGUUUG	1909
rs1065745	1499	AAACCCUGACCGCAGUCGG	158	1499	AAACCCUGACCGCAGUCGG	158	1517	CCGACUGCGGUCAGGGUUU	1910
rs1065745	1500	AACCCUGACCGCAGUCGGG	159	1500	AACCCUGACCGCAGUCGGG	159	1518	CCCGACUGCGGUCAGGGUU	1911
rs1065745	1501	ACCCUGACCGCAGUCGGGG	160	1501	ACCCUGACCGCAGUCGGGG	160	1519	CCCCGACUGCGGUCAGGGU	1912
rs1065745	1502	CCUGACCGCAGUCGGGGG	161	1502	CCUGACCGCAGUCGGGGG	161	1520	CCCCGACUGCGGUCAGGG	1913
rs1065745	1503	CCUGACCGCAGUCGGGGGC	162	1503	CCUGACCGCAGUCGGGGGC	162	1521	GCCCCGACUGCGGUCAGG	1914
rs1065745	1504	CUGACCGCAGUCGGGGGCA	163	1504	CUGACCGCAGUCGGGGGCA	163	1522	UGCCCCGACUGCGGUCAG	1915
rs1065745	1505	UGACCGCAGUCGGGGGCAU	164	1505	UGACCGCAGUCGGGGGCAU	164	1523	AUGCCCCGACUGCGGGUCA	1916
rs1065745	1506	GACCGCAGUCGGGGGCAU	165	1506	GACCGCAGUCGGGGGCAU	165	1524	AAUGCCCCGACUGCGGUC	1917
rs1065745	1507	ACCGCAGUCGGGGGCAUUG	166	1507	ACCGCAGUCGGGGGCAUUG	166	1525	CAAUGCCCCGACUGCGGU	1918
rs1065745	1508	CCGCAGUCGGGGGCAUUGG	167	1508	CCGCAGUCGGGGGCAUUGG	167	1526	CCAAUGCCCCGACUGCGG	1919
rs1065745	1509	CGCAGUCGGGGGCAUUGGG	168	1509	CGCAGUCGGGGGCAUUGGG	168	1527	CCCAAUGCCCCGACUGCG	1920
rs1065745	1491	GCUUCUGCAAACCCUGACU	169	1491	GCUUCUGCAAACCCUGACU	169	1509	AGUCAGGGUUUGCAGAAGC	1921
rs1065745	1492	CUUCUGCAAACCCUGACUG	170	1492	CUUCUGCAAACCCUGACUG	170	1510	CAGUCAGGGUUUGCAGAAG	1922
rs1065745	1493	UUCUGCAAACCCUGACUGC	171	1493	UUCUGCAAACCCUGACUGC	171	1511	GCAGUCAGGGUUUGCAGAA	1923
rs1065745	1494	UCUGCAAACCCUGACUGCA	172	1494	UCUGCAAACCCUGACUGCA	172	1512	UGCAGUCAGGGUUUGCAGA	1924
rs1065745	1495	CUGCAAACCCUGACUGCAG	173	1495	CUGCAAACCCUGACUGCAG	173	1513	CUGCAGUCAGGGUUUGCAG	1925
rs1065745	1496	UGCAAACCCUGACUGCAGU	174	1496	UGCAAACCCUGACUGCAGU	174	1514	ACUGCAGUCAGGGUUUGCA	1926
rs1065745	1497	GCAAACCCUGACUGCAGUC	175	1497	GCAAACCCUGACUGCAGUC	175	1515	GACUGCAGUCAGGGUUUGC	1927
rs1065745	1498	CAAACCCUGACUGCAGUCG	176	1498	CAAACCCUGACUGCAGUCG	176	1516	CGACUGCAGUCAGGGUUUG	1928
rs1065745	1499	AAACCCUGACUGCAGUCGG	177	1499	AAACCCUGACUGCAGUCGG	177	1517	CCGACUGCAGUCAGGGUUU	1929
rs1065745	1500	AACCCUGACUGCAGUCGGG	178	1500	AACCCUGACUGCAGUCGGG	178	1518	CCCGACUGCAGUCAGGGUU	1930
rs1065745	1501	ACCCUGACUGCAGUCGGGG	179	1501	ACCCUGACUGCAGUCGGGG	179	1519	CCCCGACUGCAGUCAGGGU	1931
rs1065745	1502	CCUGACUGCAGUCGGGGG	180	1502	CCUGACUGCAGUCGGGGG	180	1520	CCCCGACUGCAGUCAGGG	1932
rs1065745	1503	CCUGACUGCAGUCGGGGGC	181	1503	CCUGACUGCAGUCGGGGGC	181	1521	GCCCCGACUGCAGUCAGG	1933
rs1065745	1504	CUGACUGCAGUCGGGGGCA	182	1504	CUGACUGCAGUCGGGGGCA	182	1522	UGCCCCGACUGCAGUCAG	1934
rs1065745	1505	UGACUGCAGUCGGGGGCAU	183	1505	UGACUGCAGUCGGGGGCAU	183	1523	AUGCCCCGACUGCAGUCA	1935
rs1065745	1506	GACUGCAGUCGGGGGCAU	184	1506	GACUGCAGUCGGGGGCAU	184	1524	AAUGCCCCGACUGCAGUC	1936
rs1065745	1507	ACUGCAGUCGGGGGCAUUG	185	1507	ACUGCAGUCGGGGGCAUUG	185	1525	CAAUGCCCCGACUGCAGU	1937
rs1065745	1508	CUGCAGUCGGGGGCAUUGG	186	1508	CUGCAGUCGGGGGCAUUGG	186	1526	CCAAUGCCCCGACUGCAG	1938
rs1065745	1509	UGCAGUCGGGGGCAUUGGG	187	1509	UGCAGUCGGGGGCAUUGGG	187	1527	CCCAAUGCCCCGACUGCAG	1939
rs2301367	1839	GGCGACUCAGUGGAUCUG	188	1839	GGCGACUCAGUGGAUCUG	188	1857	CAGAUCCACUCAGUCCGCC	1940
rs2301367	1840	GCGGACUCAGUGGAUCUGG	189	1840	GCGGACUCAGUGGAUCUGG	189	1858	CCAGAUCCACUCAGUCCGC	1941
rs2301367	1841	CGGACUCAGUGGAUCUGGC	190	1841	CGGACUCAGUGGAUCUGGC	190	1859	GCCAGAUCCACUCAGUCCG	1942
rs2301367	1842	GGACUCAGUGGAUCUGGCC	191	1842	GGACUCAGUGGAUCUGGCC	191	1860	GGCCAGAUCCACUCAGUCC	1943

rs2301367	1843	GACUCAGUGGAUCUGGCCA	192	1843	GACUCAGUGGAUCUGGCCA	192	1861	UGGCCAGAUCCACUGAGUC	1944
rs2301367	1844	ACUCAGUGGAUCUGGCCAG	193	1844	ACUCAGUGGAUCUGGCCAG	193	1862	CUGGCCAGAUCCACUGAGU	1945
rs2301367	1845	CUCAGUGGAUCUGGCCAGC	194	1845	CUCAGUGGAUCUGGCCAGC	194	1863	GCUGGCCAGAUCCACUGAG	1946
rs2301367	1846	UCAGUGGAUCUGGCCAGCU	195	1846	UCAGUGGAUCUGGCCAGCU	195	1864	AGCUGGCCAGAUCCACUGA	1947
rs2301367	1847	CAGUGGAUCUGGCCAGCUG	196	1847	CAGUGGAUCUGGCCAGCUG	196	1865	CAGCUGGCCAGAUCCACUG	1948
rs2301367	1848	AGUGGAUCUGGCCAGCUGU	197	1848	AGUGGAUCUGGCCAGCUGU	197	1866	ACAGCUGGCCAGAUCCACU	1949
rs2301367	1849	GUGGAUCUGGCCAGCUGUG	198	1849	GUGGAUCUGGCCAGCUGUG	198	1867	CACAGCUGGCCAGAUCCAC	1950
rs2301367	1850	UGGAUCUGGCCAGCUGUGA	199	1850	UGGAUCUGGCCAGCUGUGA	199	1868	UCACAGCUGGCCAGAUCCA	1951
rs2301367	1851	GGAUCUGGCCAGCUGUGAC	200	1851	GGAUCUGGCCAGCUGUGAC	200	1869	GUCACAGCUGGCCAGAUCC	1952
rs2301367	1852	GAUCUGGCCAGCUGUGACU	201	1852	GAUCUGGCCAGCUGUGACU	201	1870	AGUCACAGCUGGCCAGAU	1953
rs2301367	1853	AUCUGGCCAGCUGUGACUU	202	1853	AUCUGGCCAGCUGUGACUU	202	1871	AAGUCACAGCUGGCCAGAU	1954
rs2301367	1854	UCUGGCCAGCUGUGACUUG	203	1854	UCUGGCCAGCUGUGACUUG	203	1872	CAAGUCACAGCUGGCCAGA	1955
rs2301367	1855	CUGGCCAGCUGUGACUUGA	204	1855	CUGGCCAGCUGUGACUUGA	204	1873	UCAAGUCACAGCUGGCCAG	1956
rs2301367	1856	UGGCCAGCUGUGACUUGAC	205	1856	UGGCCAGCUGUGACUUGAC	205	1874	GUCAAGUCACAGCUGGCCA	1957
rs2301367	1857	GGCCAGCUGUGACUUGACA	206	1857	GGCCAGCUGUGACUUGACA	206	1875	UGUCAAGUCACAGCUGGCC	1958
rs2301367	1839	GGCGACUCAGUGGAUCUA	207	1839	GGCGACUCAGUGGAUCUA	207	1857	UAGAUCACUCAGAGUCCGCC	1959
rs2301367	1840	GCGGACUCAGUGGAUCUAG	208	1840	GCGGACUCAGUGGAUCUAG	208	1858	CUAGAUCACUCAGAGUCCGC	1960
rs2301367	1841	CGGACUCAGUGGAUCUAGC	209	1841	CGGACUCAGUGGAUCUAGC	209	1859	GCUAGAUCACUCAGAGUCCG	1961
rs2301367	1842	GGACUCAGUGGAUCUAGCC	210	1842	GGACUCAGUGGAUCUAGCC	210	1860	GGCUAGAUCACUCAGAGUCC	1962
rs2301367	1843	GACUCAGUGGAUCUAGCCA	211	1843	GACUCAGUGGAUCUAGCCA	211	1861	UGGCUAGAUCACUCAGAGUC	1963
rs2301367	1844	ACUCAGUGGAUCUAGCCAG	212	1844	ACUCAGUGGAUCUAGCCAG	212	1862	CUGGCUAGAUCACUCAGAGU	1964
rs2301367	1845	CUCAGUGGAUCUAGCCAGC	213	1845	CUCAGUGGAUCUAGCCAGC	213	1863	GCUGGCUAGAUCACUCAGAG	1965
rs2301367	1846	UCAGUGGAUCUAGCCAGCU	214	1846	UCAGUGGAUCUAGCCAGCU	214	1864	AGCUGGCUAGAUCACUCAGA	1966
rs2301367	1847	CAGUGGAUCUAGCCAGCUG	215	1847	CAGUGGAUCUAGCCAGCUG	215	1865	CAGCUGGCUAGAUCACUCAG	1967
rs2301367	1848	AGUGGAUCUAGCCAGCUGU	216	1848	AGUGGAUCUAGCCAGCUGU	216	1866	ACAGCUGGCUAGAUCACUC	1968
rs2301367	1849	GUGGAUCUAGCCAGCUGUG	217	1849	GUGGAUCUAGCCAGCUGUG	217	1867	CACAGCUGGCUAGAUCAC	1969
rs2301367	1850	UGGAUCUAGCCAGCUGUGA	218	1850	UGGAUCUAGCCAGCUGUGA	218	1868	UCACAGCUGGCUAGAUC	1970
rs2301367	1851	GGAUCUAGCCAGCUGUGAC	219	1851	GGAUCUAGCCAGCUGUGAC	219	1869	GUCACAGCUGGCUAGAUC	1971
rs2301367	1852	AUCUAGCCAGCUGUGACU	220	1852	AUCUAGCCAGCUGUGACU	220	1870	AGUCACAGCUGGCUAGAUC	1972
rs2301367	1853	AUCUAGCCAGCUGUGACUU	221	1853	AUCUAGCCAGCUGUGACUU	221	1871	AAGUCACAGCUGGCUAGA	1973
rs2301367	1854	UCUAGCCAGCUGUGACUUG	222	1854	UCUAGCCAGCUGUGACUUG	222	1872	CAAGUCACAGCUGGCUAGA	1974
rs2301367	1855	CUAGCCAGCUGUGACUUGA	223	1855	CUAGCCAGCUGUGACUUGA	223	1873	UCAAGUCACAGCUGGCUAG	1975
rs2301367	1856	UAGCCAGCUGUGACUUGAC	224	1856	UAGCCAGCUGUGACUUGAC	224	1874	GUCAAGUCACAGCUGGCUA	1976
rs2301367	1857	AGCCAGCUGUGACUUGACA	225	1857	AGCCAGCUGUGACUUGACA	225	1875	UGUCAAGUCACAGCUGGCU	1977
rs363075	2980	GCAGAAACUUACACAGAG	226	2980	GCAGAAACUUACACAGAG	226	2998	CUCUGUGAAAGUUUUCUG	1978
rs363075	2981	CAGAAACUUACACAGAGG	227	2981	CAGAAACUUACACAGAGG	227	2999	CCUCUGUGAAAGUUUUCUG	1979
rs363075	2982	AGAAACUUACACAGAGGG	228	2982	AGAAACUUACACAGAGGG	228	3000	CCCUCUGUGAAAGUUUUCU	1980
rs363075	2983	GAAACUUACACAGAGGGG	229	2983	GAAACUUACACAGAGGGG	229	3001	CCCCUCUGUGAAAGUUUUC	1981
rs363075	2984	AAACUUACACAGAGGGGC	230	2984	AAACUUACACAGAGGGGC	230	3002	GCCCCUCUGUGAAAGUUUU	1982

rs363075	2985	AAACUUACACAGAGGGGCU	231	2985	AAACUUACACAGAGGGGCU	231	3003	AGCCCCUCUGUAAAGUUU	1983
rs363075	2986	AACUUACACAGAGGGGCU	232	2986	AACUUACACAGAGGGGCU	232	3004	GAGCCCCUCUGUAAAGUU	1984
rs363075	2987	ACUUACACAGAGGGGCUA	233	2987	ACUUACACAGAGGGGCUA	233	3005	UGAGCCCCUCUGUAAAGU	1985
rs363075	2988	CUUACACAGAGGGGCUCAU	234	2988	CUUACACAGAGGGGCUCAU	234	3006	AUGAGCCCCUCUGUGUAA	1986
rs363075	2989	UUACACAGAGGGGCUCAUC	235	2989	UUACACAGAGGGGCUCAUC	235	3007	GAUGAGCCCCUCUGUGUAA	1987
rs363075	2990	UACACAGAGGGGCUCAUCA	236	2990	UACACAGAGGGGCUCAUCA	236	3008	UGAUGAGCCCCUCUGUGUA	1988
rs363075	2991	ACACAGAGGGGCUCAUCAU	237	2991	ACACAGAGGGGCUCAUCAU	237	3009	AUGAUGAGCCCCUCUGUGU	1989
rs363075	2992	CACAGAGGGGCUCAUCAUU	238	2992	CACAGAGGGGCUCAUCAUU	238	3010	AAUGAUGAGCCCCUCUGUG	1990
rs363075	2993	ACAGAGGGGCUCAUCAUUA	239	2993	ACAGAGGGGCUCAUCAUUA	239	3011	UAAUGAUGAGCCCCUCUGU	1991
rs363075	2994	CAGAGGGGCUCAUCAUUUA	240	2994	CAGAGGGGCUCAUCAUUUA	240	3012	AUAUGAUGAGCCCCUCUG	1992
rs363075	2995	AGAGGGGCUCAUCAUUUA	241	2995	AGAGGGGCUCAUCAUUUA	241	3013	UAUAUGAUGAGCCCCUCUC	1993
rs363075	2996	GAGGGGCUCAUCAUUUAUC	242	2996	GAGGGGCUCAUCAUUUAUC	242	3014	GUUAUAUGAUGAGCCCCUC	1994
rs363075	2997	AGGGGCUCAUCAUUUAACA	243	2997	AGGGGCUCAUCAUUUAACA	243	3015	UGUAUAUGAUGAGCCCCUC	1995
rs363075	2998	GGGGCUCAUCAUUUAACAG	244	2998	GGGGCUCAUCAUUUAACAG	244	3016	CUGUAUAUGAUGAGCCCCC	1996
rs363075	2980	GCAGAAACUUACACAGAA	245	2980	GCAGAAACUUACACAGAA	245	2998	UUCUGUGUAAAGUUUUCGC	1997
rs363075	2981	CAGAAACUUACACAGAAG	246	2981	CAGAAACUUACACAGAAG	246	2999	CUUCUGUGUAAAGUUUUCUG	1998
rs363075	2982	AGAAACUUACACAGAAGG	247	2982	AGAAACUUACACAGAAGG	247	3000	CCUUCUGUGUAAAGUUUUCU	1999
rs363075	2983	GAAACUUACACAGAAGGG	248	2983	GAAACUUACACAGAAGGG	248	3001	CCCUUCUGUGUAAAGUUUUC	2000
rs363075	2984	AAACUUACACAGAAGGGC	249	2984	AAACUUACACAGAAGGGC	249	3002	GCCCUUCUGUGUAAAGUUUU	2001
rs363075	2985	AAACUUACACAGAAGGGCU	250	2985	AAACUUACACAGAAGGGCU	250	3003	AGCCCUUCUGUGUAAAGUUU	2002
rs363075	2986	AACUUACACAGAAGGGGCU	251	2986	AACUUACACAGAAGGGGCU	251	3004	GAGCCCUUCUGUGUAAAGUU	2003
rs363075	2987	ACUUACACAGAAGGGGCUA	252	2987	ACUUACACAGAAGGGGCUA	252	3005	UGAGCCCUUCUGUGUAAAGU	2004
rs363075	2988	CUUACACAGAAGGGGCUCAU	253	2988	CUUACACAGAAGGGGCUCAU	253	3006	AUGAGCCCUUCUGUGUAAAG	2005
rs363075	2989	UUACACAGAAGGGGCUCAUC	254	2989	UUACACAGAAGGGGCUCAUC	254	3007	GAUGAGCCCUUCUGUGUAA	2006
rs363075	2990	UACACAGAAGGGGCUCAUCA	255	2990	UACACAGAAGGGGCUCAUCA	255	3008	UGAUGAGCCCUUCUGUGUA	2007
rs363075	2991	ACACAGAAGGGGCUCAUCAU	256	2991	ACACAGAAGGGGCUCAUCAU	256	3009	AUGAUGAGCCCUUCUGUGU	2008
rs363075	2992	CACAGAAGGGGCUCAUCAUU	257	2992	CACAGAAGGGGCUCAUCAUU	257	3010	AAUGAUGAGCCCUUCUGUG	2009
rs363075	2993	ACAGAAGGGGCUCAUCAUUA	258	2993	ACAGAAGGGGCUCAUCAUUA	258	3011	UAAUGAUGAGCCCUUCUGU	2010
rs363075	2994	CAGAAGGGGCUCAUCAUUUA	259	2994	CAGAAGGGGCUCAUCAUUUA	259	3012	AUAUGAUGAGCCCUUCUG	2011
rs363075	2995	AGAAGGGGCUCAUCAUUUA	260	2995	AGAAGGGGCUCAUCAUUUA	260	3013	UAUAUGAUGAGCCCUUCUC	2012
rs363075	2996	GAAGGGGCUCAUCAUUUAUC	261	2996	GAAGGGGCUCAUCAUUUAUC	261	3014	GUUAUAUGAUGAGCCCUUC	2013
rs363075	2997	AAGGGGCUCAUCAUUUAACA	262	2997	AAGGGGCUCAUCAUUUAACA	262	3015	UGUAUAUGAUGAGCCCUUC	2014
rs363075	2998	AGGGGCUCAUCAUUUAACAG	263	2998	AGGGGCUCAUCAUUUAACAG	263	3016	CUGUAUAUGAUGAGCCCUUC	2015
rs1065746	3547	UCAGCUUGGUUCCCAUUGG	264	3547	UCAGCUUGGUUCCCAUUGG	264	3565	CCAAUGGGAACCAAGCUGA	2016
rs1065746	3548	CAGCUUGGUUCCCAUUGGA	265	3548	CAGCUUGGUUCCCAUUGGA	265	3566	UCCAAUGGGAACCAAGCUG	2017
rs1065746	3549	AGCUUGGUUCCCAUUGGAU	266	3549	AGCUUGGUUCCCAUUGGAU	266	3567	AUCCAAUGGGAACCAAGCU	2018
rs1065746	3550	GCUUGGUUCCCAUUGGAUC	267	3550	GCUUGGUUCCCAUUGGAUC	267	3568	GAUCCAAUGGGAACCAAGC	2019
rs1065746	3551	CUUGGUUCCCAUUGGAUCU	268	3551	CUUGGUUCCCAUUGGAUCU	268	3569	AGAUCCAAUGGGAACCAAG	2020
rs1065746	3552	UUGGUUCCCAUUGGAUCUC	269	3552	UUGGUUCCCAUUGGAUCUC	269	3570	GAGAUCCAAUGGGAACCAAA	2021

rs1065746	3553	UGGUUCCCAUUGGAUCUCU	270	3553	UGGUUCCCAUUGGAUCUCU	270	3571	AGAGAUCCAAUUGGGAACCA	2022
rs1065746	3554	GGUUCCCAUUGGAUCUCUC	271	3554	GGUUCCCAUUGGAUCUCUC	271	3572	GAGAGAUCCAAUUGGGAACC	2023
rs1065746	3555	GUUCCCAUUGGAUCUCUCA	272	3555	GUUCCCAUUGGAUCUCUCA	272	3573	UGAGAGAUCCAAUUGGGAAC	2024
rs1065746	3556	UUCCCAUIUGGAUCUCUCAG	273	3556	UUCCCAUIUGGAUCUCUCAG	273	3574	CUGAGAGAUCCAAUUGGGAA	2025
rs1065746	3557	UCCCAUIUGGAUCUCUCAGC	274	3557	UCCCAUIUGGAUCUCUCAGC	274	3575	GCUGAGAGAUCCAAUUGGGA	2026
rs1065746	3558	CCCAUIUGGAUCUCUCAGGCC	275	3558	CCCAUIUGGAUCUCUCAGGCC	275	3576	GGCUGAGAGAUCCAAUUGGG	2027
rs1065746	3559	CCAUIUGGAUCUCUCAGGCC	276	3559	CCAUIUGGAUCUCUCAGGCC	276	3577	GGGCUGAGAGAUCCAAUUGG	2028
rs1065746	3560	CAUUGGAUCUCUCAGGCCA	277	3560	CAUUGGAUCUCUCAGGCCA	277	3578	UGGGCUGAGAGAUCCAAUUG	2029
rs1065746	3561	AUUGGAUCUCUCAGGCCAU	278	3561	AUUGGAUCUCUCAGGCCAU	278	3579	AUGGGCUGAGAGAUCCAAU	2030
rs1065746	3562	UUGGAUCUCUCAGGCCAU	279	3562	UUGGAUCUCUCAGGCCAU	279	3580	GAUGGGCUGAGAGAUCCAA	2031
rs1065746	3563	UGGAUCUCUCAGGCCAU	280	3563	UGGAUCUCUCAGGCCAU	280	3581	UGAUGGGCUGAGAGAUCCA	2032
rs1065746	3564	GGAUCUCUCAGGCCAUCAA	281	3564	GGAUCUCUCAGGCCAUCAA	281	3582	UUGAUGGGCUGAGAGAUCC	2033
rs1065746	3565	GAUCUCUCAGGCCAUCAA	282	3565	GAUCUCUCAGGCCAUCAA	282	3583	CUUGAUGGGCUGAGAGAUCC	2034
rs1065746	3547	UCAGCUUGGUUCCCAUUGA	283	3547	UCAGCUUGGUUCCCAUUGA	283	3565	UCAAUUGGGAACCAAGCUGA	2035
rs1065746	3548	CAGCUUGGUUCCCAUUGAA	284	3548	CAGCUUGGUUCCCAUUGAA	284	3566	UUCAUUGGGAACCAAGCUG	2036
rs1065746	3549	AGCUUGGUUCCCAUUGAAU	285	3549	AGCUUGGUUCCCAUUGAAU	285	3567	AUUCAUUGGGAACCAAGCU	2037
rs1065746	3550	GCUUGGUUCCCAUUGAAUC	286	3550	GCUUGGUUCCCAUUGAAUC	286	3568	GAUUCAUUGGGAACCAAGC	2038
rs1065746	3551	CUUGGUUCCCAUUGAAUCU	287	3551	CUUGGUUCCCAUUGAAUCU	287	3569	AGAUUCAUUGGGAACCAAG	2039
rs1065746	3552	UUGGUUCCCAUUGAAUCUC	288	3552	UUGGUUCCCAUUGAAUCUC	288	3570	GAGAUUCAUUGGGAACCAA	2040
rs1065746	3553	UGGUUCCCAUUGAAUCUCU	289	3553	UGGUUCCCAUUGAAUCUCU	289	3571	AGAGAUUCAUUGGGAACCA	2041
rs1065746	3554	GGUUCCCAUUGAAUCUCUC	290	3554	GGUUCCCAUUGAAUCUCUC	290	3572	GAGAGAUUCAUUGGGAACC	2042
rs1065746	3555	GUUCCCAUUGAAUCUCUCA	291	3555	GUUCCCAUUGAAUCUCUCA	291	3573	UGAGAGAUUCAUUGGGAAC	2043
rs1065746	3556	UUCCCAUIUGAAUCUCUCAG	292	3556	UUCCCAUIUGAAUCUCUCAG	292	3574	CUGAGAGAUUCAUUGGGAA	2044
rs1065746	3557	UCCCAUIUGAAUCUCUCAGC	293	3557	UCCCAUIUGAAUCUCUCAGC	293	3575	GCUGAGAGAUUCAUUGGGA	2045
rs1065746	3558	CCCAUUGAAUCUCUCAGGCC	294	3558	CCCAUUGAAUCUCUCAGGCC	294	3576	GGCUGAGAGAUUCAUUGGG	2046
rs1065746	3559	CCAUUGAAUCUCUCAGGCC	295	3559	CCAUUGAAUCUCUCAGGCC	295	3577	GGGCUGAGAGAUUCAUUGG	2047
rs1065746	3560	CAUUGAAUCUCUCAGGCCA	296	3560	CAUUGAAUCUCUCAGGCCA	296	3578	UGGGCUGAGAGAUUCAUUG	2048
rs1065746	3561	AUUGAAUCUCUCAGGCCAU	297	3561	AUUGAAUCUCUCAGGCCAU	297	3579	AUGGGCUGAGAGAUUCAAU	2049
rs1065746	3562	UUGAAUCUCUCAGGCCAU	298	3562	UUGAAUCUCUCAGGCCAU	298	3580	GAUGGGCUGAGAGAUUCA	2050
rs1065746	3563	UGAAUCUCUCAGGCCAU	299	3563	UGAAUCUCUCAGGCCAU	299	3581	UGAUGGGCUGAGAGAUUCA	2051
rs1065746	3564	GAUCUCUCAGGCCAUCAA	300	3564	GAUCUCUCAGGCCAUCAA	300	3582	UUGAUGGGCUGAGAGAUUC	2052
rs1065746	3565	AAUCUCUCAGGCCAUCAA	301	3565	AAUCUCUCAGGCCAUCAA	301	3583	CUUGAUGGGCUGAGAGAUU	2053
rs1065746	3547	UCAGCUUGGUUCCCAUUGC	302	3547	UCAGCUUGGUUCCCAUUGC	302	3565	GCAAUGGGAACCAAGCUGA	2054
rs1065746	3548	CAGCUUGGUUCCCAUUGCA	303	3548	CAGCUUGGUUCCCAUUGCA	303	3566	UGCAAUGGGAACCAAGCUG	2055
rs1065746	3549	AGCUUGGUUCCCAUUGCAU	304	3549	AGCUUGGUUCCCAUUGCAU	304	3567	AUGCAAUGGGAACCAAGCU	2056
rs1065746	3550	GCUUGGUUCCCAUUGCAUC	305	3550	GCUUGGUUCCCAUUGCAUC	305	3568	GAUGCAAUGGGAACCAAGC	2057
rs1065746	3551	CUUGGUUCCCAUUGCAUCU	306	3551	CUUGGUUCCCAUUGCAUCU	306	3569	AGAUGCAAUGGGAACCAAG	2058
rs1065746	3552	UUGGUUCCCAUUGCAUCUC	307	3552	UUGGUUCCCAUUGCAUCUC	307	3570	GAGAUGCAAUGGGAACCAA	2059
rs1065746	3553	UGGUUCCCAUUGCAUCUCU	308	3553	UGGUUCCCAUUGCAUCUCU	308	3571	AGAGAUCCAAUUGGGAACCA	2060

rs1065746	3554	GGUCCCCAUUGCAUCUCUC	309	3554	GGUCCCCAUUGCAUCUCUC	309	3572	GAGAGAUGCAAUGGGAACC	2061
rs1065746	3555	GUUCCCCAUUGCAUCUCUCA	310	3555	GUUCCCCAUUGCAUCUCUCA	310	3573	UGAGAUGCAAUGGGAAC	2062
rs1065746	3556	UUCCCCAUUGCAUCUCUCAG	311	3556	UUCCCCAUUGCAUCUCUCAG	311	3574	CUGAGAUGCAAUGGGAA	2063
rs1065746	3557	UCCCAUUGCAUCUCUCAGC	312	3557	UCCCAUUGCAUCUCUCAGC	312	3575	GCUGAGAUGCAAUGGGA	2064
rs1065746	3558	CCCAUUGCAUCUCUCAGGCC	313	3558	CCCAUUGCAUCUCUCAGGCC	313	3576	GGCUGAGAUGCAAUGGG	2065
rs1065746	3559	CCAUUGCAUCUCUCAGGCC	314	3559	CCAUUGCAUCUCUCAGGCC	314	3577	GGCUGAGAUGCAAUGG	2066
rs1065746	3560	CAUUGCAUCUCUCAGGCCA	315	3560	CAUUGCAUCUCUCAGGCCA	315	3578	UGGCUGAGAUGCAAUG	2067
rs1065746	3561	AUUGCAUCUCUCAGGCCAU	316	3561	AUUGCAUCUCUCAGGCCAU	316	3579	AUGGCUGAGAUGCAAU	2068
rs1065746	3562	UUGCAUCUCUCAGGCCAUC	317	3562	UUGCAUCUCUCAGGCCAUC	317	3580	GAUGGCUGAGAUGCAA	2069
rs1065746	3563	UGCAUCUCUCAGGCCAUA	318	3563	UGCAUCUCUCAGGCCAUA	318	3581	UGAUGGCUGAGAUGCA	2070
rs1065746	3564	GCAUCUCUCAGGCCCAUAA	319	3564	GCAUCUCUCAGGCCCAUAA	319	3582	UUGAUGGCUGAGAUGC	2071
rs1065746	3565	CAUCUCUCAGGCCCAUAG	320	3565	CAUCUCUCAGGCCCAUAG	320	3583	CUUGAUGGCUGAGAUG	2072
rs1065746	3647	GGCCUCUGAAGAAAGAAC	321	3647	GGCCUCUGAAGAAAGAAC	321	3665	GCUCUCUCUCAGAGGCC	2073
rs1065747	3648	GGCCUCUGAAGAAAGAAC	322	3648	GGCCUCUGAAGAAAGAAC	322	3666	GGCUCUCUCUCAGAGGCC	2074
rs1065747	3649	GGCUCUGAAGAAAGAACCA	323	3649	GGCUCUGAAGAAAGAACCA	323	3667	UGCUCUCUCUCAGAGGC	2075
rs1065747	3650	CCUCUGAAGAAAGAACCA	324	3650	CCUCUGAAGAAAGAACCA	324	3668	UUGCUCUCUCUCAGAGG	2076
rs1065747	3651	CUCUGAAGAAAGAACCAAC	325	3651	CUCUGAAGAAAGAACCAAC	325	3669	GUUGCUCUCUCUCAGAG	2077
rs1065747	3652	UCUGAAGAAAGAACCAACC	326	3652	UCUGAAGAAAGAACCAACC	326	3670	GGUUGCUCUCUCUCAGA	2078
rs1065747	3653	CUGAAGAAAGAACCAACCC	327	3653	CUGAAGAAAGAACCAACCC	327	3671	GGUUGCUCUCUCUCUCAG	2079
rs1065747	3654	UGAAGAAAGAACCAACCCA	328	3654	UGAAGAAAGAACCAACCCA	328	3672	UGGUUGGCUCUCUCUCA	2080
rs1065747	3655	GAAGAAGAACCAACCCAG	329	3655	GAAGAAGAACCAACCCAG	329	3673	CUGGUUGGCUCUCUCUUC	2081
rs1065747	3656	AAGAAGAACCAACCCAGC	330	3656	AAGAAGAACCAACCCAGC	330	3674	GCUGGUUGGCUCUCUCUU	2082
rs1065747	3657	AGAAGAACCAACCCAGCA	331	3657	AGAAGAACCAACCCAGCA	331	3675	UGCUGGUUGGCUCUCUCU	2083
rs1065747	3658	GAAGAAGCAACCCAGCAG	332	3658	GAAGAAGCAACCCAGCAG	332	3676	CUGCUGGUUGGCUCUCUC	2084
rs1065747	3659	AAGAAGCAACCCAGCAGC	333	3659	AAGAAGCAACCCAGCAGC	333	3677	GCUGCUGGUUGGCUCUCU	2085
rs1065747	3660	AGAAGCAACCCAGCAGCC	334	3660	AGAAGCAACCCAGCAGCC	334	3678	GGCUGCUGGUUGGCUCUCU	2086
rs1065747	3661	GAAGCAACCCAGCAGCCA	335	3661	GAAGCAACCCAGCAGCCA	335	3679	UGGCUGCUGGUUGGCUCUC	2087
rs1065747	3662	AAGCAACCCAGCAGCCAC	336	3662	AAGCAACCCAGCAGCCAC	336	3680	GUGGCUGCUGGUUGGCUCU	2088
rs1065747	3663	AGCAACCCAGCAGCCACC	337	3663	AGCAACCCAGCAGCCACC	337	3681	UGGCUGCUGGUUGGCUCU	2089
rs1065747	3664	GCAACCCAGCAGCCACCA	338	3664	GCAACCCAGCAGCCACCA	338	3682	UGGUUGGCUGGUUGGCUCU	2090
rs1065747	3665	CCAACCCAGCAGCCACCAA	339	3665	CCAACCCAGCAGCCACCAA	339	3683	UUGGUUGGCUGGUUGGCUCU	2091
rs1065747	3647	GGCCUCUGAAGAAAGAGG	340	3647	GGCCUCUGAAGAAAGAGG	340	3665	CCUUCUCUCUCAGAGGCC	2092
rs1065747	3648	GGCCUCUGAAGAAAGAGGC	341	3648	GGCCUCUGAAGAAAGAGGC	341	3666	GCCUUCUCUCUCAGAGGCC	2093
rs1065747	3649	GCCUCUGAAGAAAGAGGCA	342	3649	GCCUCUGAAGAAAGAGGCA	342	3667	UGCCUUCUCUCUCAGAGGC	2094
rs1065747	3650	CCUCUGAAGAAAGAGGCAA	343	3650	CCUCUGAAGAAAGAGGCAA	343	3668	UUGCCUUCUCUCUCAGAGG	2095
rs1065747	3651	CUCUGAAGAAAGAGGCAAC	344	3651	CUCUGAAGAAAGAGGCAAC	344	3669	GUUGCCUUCUCUCUCAGAG	2096
rs1065747	3652	UCUGAAGAAAGAGGCAACC	345	3652	UCUGAAGAAAGAGGCAACC	345	3670	GGUUGCCUUCUCUCUCAGA	2097
rs1065747	3653	CUGAAGAAAGAGGCAACCC	346	3653	CUGAAGAAAGAGGCAACCC	346	3671	GGGUUGCCUUCUCUCUCAG	2098
rs1065747	3654	UGAAGAAAGAGGCAACCCA	347	3654	UGAAGAAAGAGGCAACCCA	347	3672	UGGUUGCCUUCUCUCUCA	2099

rs1065747	3655	GAAGAAGGCAACCCAG	348	3655	GAAGAAGGCAACCCAG	348	3673	CUGGGUUGCCUUCUUCUUC	2100
rs1065747	3656	AAGAAGAGGCAACCCAGC	349	3656	AAGAAGAGGCAACCCAGC	349	3674	GCUGGGUUGCCUUCUUCUU	2101
rs1065747	3657	AGAAGAAGGCAACCCAGCA	350	3657	AGAAGAAGGCAACCCAGCA	350	3675	UGCUGGGUUGCCUUCUUCU	2102
rs1065747	3658	GAAGAAGGCAACCCAGCAG	351	3658	GAAGAAGGCAACCCAGCAG	351	3676	CUGCUGGGUUGCCUUCUUC	2103
rs1065747	3659	AAGAAGGCAACCCAGCAGC	352	3659	AAGAAGGCAACCCAGCAGC	352	3677	GCUGCUGGGUUGCCUUCUU	2104
rs1065747	3660	AGAAGGCAACCCAGCAGCC	353	3660	AGAAGGCAACCCAGCAGCC	353	3678	GGCUGCUGGGUUGCCUUCU	2105
rs1065747	3661	GAAGGCAACCCAGCAGCCA	354	3661	GAAGGCAACCCAGCAGCCA	354	3679	UGGCUGCUGGGUUGCCUUC	2106
rs1065747	3662	AAGGCAACCCAGCAGCCAC	355	3662	AAGGCAACCCAGCAGCCAC	355	3680	GUGGCUGCUGGGUUGCCUU	2107
rs1065747	3663	AGGCAACCCAGCAGCCACC	356	3663	AGGCAACCCAGCAGCCACC	356	3681	GGUGGCUGCUGGGUUGCCU	2108
rs1065747	3664	GGCAACCCAGCAGCCACCA	357	3664	GGCAACCCAGCAGCCACCA	357	3682	UGUGGCUGCUGGGUUGGCC	2109
rs1065747	3665	GCAACCCAGCAGCCACCAA	358	3665	GCAACCCAGCAGCCACCAA	358	3683	UUGGUGGCUGCUGGGUUGC	2110
rs2530588	3803	CUGACCCCGCAUAAAGGC	359	3803	CUGACCCCGCAUAAAGGC	359	3821	GCCUUUUAUUGCGGGUCCAG	2111
rs2530588	3804	UGGACCCGCAUAAAGGCA	360	3804	UGGACCCGCAUAAAGGCA	360	3822	UGCCUUUUAUUGCGGGUCCA	2112
rs2530588	3805	GGACCCGCAUAAAGGCAG	361	3805	GGACCCGCAUAAAGGCAG	361	3823	CUGCCUUUUAUUGCGGGUCC	2113
rs2530588	3806	GACCCGCAUAAAGGCAGC	362	3806	GACCCGCAUAAAGGCAGC	362	3824	GCUGCCUUUUAUUGCGGGUC	2114
rs2530588	3807	ACCCGCAUAAAGGCAGCC	363	3807	ACCCGCAUAAAGGCAGCC	363	3825	GGCUGCCUUUUAUUGCGGGU	2115
rs2530588	3808	CCCGCAUAAAGGCAGCCU	364	3808	CCCGCAUAAAGGCAGCCU	364	3826	AGGCUGCCUUUUAUUGCGGG	2116
rs2530588	3809	CCGCAUAAAGGCAGCCUU	365	3809	CCGCAUAAAGGCAGCCUU	365	3827	AAGGCUGCCUUUUAUUGCGG	2117
rs2530588	3810	CGCAUAAAGGCAGCCUUG	366	3810	CGCAUAAAGGCAGCCUUG	366	3828	CAAGGCUGCCUUUUAUUGCG	2118
rs2530588	3811	GCAUAAAGGCAGCCUUGC	367	3811	GCAUAAAGGCAGCCUUGC	367	3829	GCAAGGCUGCCUUUUAUUGC	2119
rs2530588	3812	CAUAAAGGCAGCCUUGCC	368	3812	CAUAAAGGCAGCCUUGCC	368	3830	GGCAAGGCUGCCUUUUAUUG	2120
rs2530588	3813	AUAAAGGCAGCCUUGCCU	369	3813	AUAAAGGCAGCCUUGCCU	369	3831	AGGCAAGGCUGCCUUUUAU	2121
rs2530588	3814	AUAAAGGCAGCCUUGCCUU	370	3814	AUAAAGGCAGCCUUGCCUU	370	3832	AAGGCAAGGCUGCCUUUAU	2122
rs2530588	3815	UAAAGGCAGCCUUGCCUUC	371	3815	UAAAGGCAGCCUUGCCUUC	371	3833	GAAGGCAAGGCUGCCUUUA	2123
rs2530588	3816	AAAGGCAGCCUUGCCUUCU	372	3816	AAAGGCAGCCUUGCCUUCU	372	3834	AGAAGGCAAGGCUGCCUUU	2124
rs2530588	3817	AAGGCAGCCUUGCCUUCUC	373	3817	AAGGCAGCCUUGCCUUCUC	373	3835	GAGAAGGCAAGGCUGCCUU	2125
rs2530588	3818	AGGCAGCCUUGCCUUCUCU	374	3818	AGGCAGCCUUGCCUUCUCU	374	3836	AGAGAAGGCAAGGCUGCCU	2126
rs2530588	3819	GGCAGCCUUGCCUUCUCUA	375	3819	GGCAGCCUUGCCUUCUCUA	375	3837	UAGAGAAGGCAAGGCUGCC	2127
rs2530588	3820	GCAGCCUUGCCUUCUCUAA	376	3820	GCAGCCUUGCCUUCUCUAA	376	3838	UAGAGAAGGCAAGGCUGC	2128
rs2530588	3821	CAGCCUUGCCUUCUCUAAC	377	3821	CAGCCUUGCCUUCUCUAAC	377	3839	GUAGAGAAGGCAAGGCUG	2129
rs2530588	3803	CUGGACCCGCAUAAAGGA	378	3803	CUGGACCCGCAUAAAGGA	378	3821	UCCUUUUAUUGCGGGUCCAG	2130
rs2530588	3804	UGGACCCGCAUAAAGGAA	379	3804	UGGACCCGCAUAAAGGAA	379	3822	UCCUUUUAUUGCGGGUCCA	2131
rs2530588	3805	GGACCCGCAUAAAGGAAG	380	3805	GGACCCGCAUAAAGGAAG	380	3823	CUUCCUUUUAUUGCGGGUCC	2132
rs2530588	3806	GACCCGCAUAAAGGAAGC	381	3806	GACCCGCAUAAAGGAAGC	381	3824	GCUCCUUUUAUUGCGGGUC	2133
rs2530588	3807	ACCCGCAUAAAGGAAGCC	382	3807	ACCCGCAUAAAGGAAGCC	382	3825	GGCUCCUUUUAUUGCGGGU	2134
rs2530588	3808	CCCGCAUAAAGGAAGCCU	383	3808	CCCGCAUAAAGGAAGCCU	383	3826	AGGCUCCUUUUAUUGCGGG	2135
rs2530588	3809	CCGCAUAAAGGAAGCCUU	384	3809	CCGCAUAAAGGAAGCCUU	384	3827	AAGGCUCCUUUUAUUGCGG	2136
rs2530588	3810	CGCAUAAAGGAAGCCUUG	385	3810	CGCAUAAAGGAAGCCUUG	385	3828	CAAGGCUCCUUUUAUUGCG	2137
rs2530588	3811	GCAUAAAGGAAGCCUUGC	386	3811	GCAUAAAGGAAGCCUUGC	386	3829	GCAAGGCUCCUUUUAUUGC	2138

rs2530588	3812	CAUAAAGGAAGCCUUGCC	387	3812	CAUAAAGGAAGCCUUGCC	387	3830	GGCAAGGCUUCCUUAUUG	2139
rs2530588	3813	AUAAAGGAAGCCUUGCCU	388	3813	AUAAAGGAAGCCUUGCCU	388	3831	AGGCAAGGCUUCCUUAU	2140
rs2530588	3814	AUAAAGGAAGCCUUGCCU	389	3814	AUAAAGGAAGCCUUGCCU	389	3832	AAGCAAGGCUUCCUUAU	2141
rs2530588	3815	UAAAGGAAGCCUUGCCUUC	390	3815	UAAAGGAAGCCUUGCCUUC	390	3833	GAAGCAAGGCUUCCUUA	2142
rs2530588	3816	AAAGGAAGCCUUGCCUUCU	391	3816	AAAGGAAGCCUUGCCUUCU	391	3834	AGAAGGCAAGGCUUCCU	2143
rs2530588	3817	AAGGAAGCCUUGCCUUCUC	392	3817	AAGGAAGCCUUGCCUUCUC	392	3835	GAGAAGGCAAGGCUUCCU	2144
rs2530588	3818	AGGAAGCCUUGCCUUCUCU	393	3818	AGGAAGCCUUGCCUUCUCU	393	3836	AGAGAAGGCAAGGCUUCCU	2145
rs2530588	3819	GGAAGCCUUGCCUUCUCUA	394	3819	GGAAGCCUUGCCUUCUCUA	394	3837	UAGAGAAGGCAAGGCUUCC	2146
rs2530588	3820	GAAGCCUUGCCUUCUCUAA	395	3820	GAAGCCUUGCCUUCUCUAA	395	3838	UUAGAGAAGGCAAGGCUUC	2147
rs2530588	3821	AAGCCUUGCCUUCUCUAAC	396	3821	AAGCCUUGCCUUCUCUAAC	396	3839	GUUAGAGAAGGCAAGGCUU	2148
rs3025843	3822	AGCCUUGCCUUCUCUAACA	397	3822	AGCCUUGCCUUCUCUAACA	397	3840	UGUUAGAGAAGGCAAGGCU	2149
rs3025843	3823	GCCUUGCCUUCUCUAACAA	398	3823	GCCUUGCCUUCUCUAACAA	398	3841	UUUUAGAGAAGGCAAGGC	2150
rs3025843	3824	CCUUGCCUUCUCUAACAAA	399	3824	CCUUGCCUUCUCUAACAAA	399	3842	UUUUAGAGAAGGCAAGG	2151
rs3025843	3825	CUUGCCUUCUCUAACAAAC	400	3825	CUUGCCUUCUCUAACAAAC	400	3843	GUUUAGAGAAGGCAAG	2152
rs3025843	3826	UUGCCUUCUCUAACAAACC	401	3826	UUGCCUUCUCUAACAAACC	401	3844	GGUUAGAGAAGGCAAG	2153
rs3025843	3827	UGCCUUCUCUAACAAACCC	402	3827	UGCCUUCUCUAACAAACCC	402	3845	GGUUAGAGAAGGCAAGGCA	2154
rs3025843	3828	GCCUUCUCUAACAAACCCC	403	3828	GCCUUCUCUAACAAACCCC	403	3846	GGGGUUUAGAGAAGGC	2155
rs3025843	3829	CCUUCUCUAACAAACCCCC	404	3829	CCUUCUCUAACAAACCCCC	404	3847	GGGGUUUAGAGAAGGC	2156
rs3025843	3830	CUUCUCUAACAAACCCCCC	405	3830	CUUCUCUAACAAACCCCCC	405	3848	GGGGUUUAGAGAAGGC	2157
rs3025843	3831	UUCUCUAACAAACCCCCCU	406	3831	UUCUCUAACAAACCCCCCU	406	3849	AGGGGGUUUAGAGAAG	2158
rs3025843	3832	UCUCUAACAAACCCCCCUU	407	3832	UCUCUAACAAACCCCCCUU	407	3850	AAGGGGGUUUAGAGA	2159
rs3025843	3833	CUCUAACAAACCCCCCUUC	408	3833	CUCUAACAAACCCCCCUUC	408	3851	GAAGGGGGUUUAGAGA	2160
rs3025843	3834	UCUAACAAACCCCCCUUCU	409	3834	UCUAACAAACCCCCCUUCU	409	3852	AGAAGGGGGUUUAGAGA	2161
rs3025843	3835	CUAACAAACCCCCCUUCUC	410	3835	CUAACAAACCCCCCUUCUC	410	3853	GAGAAGGGGGUUUAGAGA	2162
rs3025843	3836	UAACAAACCCCCCUUCUCU	411	3836	UAACAAACCCCCCUUCUCU	411	3854	AGAGAAGGGGGUUUAGAGA	2163
rs3025843	3837	AACAAACCCCCCUUCUCUA	412	3837	AACAAACCCCCCUUCUCUA	412	3855	UAGAGAAGGGGGUUUAGAGA	2164
rs3025843	3838	ACAAACCCCCCUUCUCUAA	413	3838	ACAAACCCCCCUUCUCUAA	413	3856	UUAGAGAAGGGGGUUUAGAGA	2165
rs3025843	3820	GCAGCCUUGCCUUCUCUAG	414	3820	GCAGCCUUGCCUUCUCUAG	414	3838	CUAGAGAAGGCAAGGCU	2166
rs3025843	3821	CAGCCUUGCCUUCUCUAGC	415	3821	CAGCCUUGCCUUCUCUAGC	415	3839	GCUAGAGAAGGCAAGGCU	2167
rs3025843	3822	AGCCUUGCCUUCUCUAGCA	416	3822	AGCCUUGCCUUCUCUAGCA	416	3840	UGCUAGAGAAGGCAAGGCU	2168
rs3025843	3823	GCCUUGCCUUCUCUAGCAA	417	3823	GCCUUGCCUUCUCUAGCAA	417	3841	UUGCUAGAGAAGGCAAGGC	2169
rs3025843	3824	CCUUGCCUUCUCUAGCAAA	418	3824	CCUUGCCUUCUCUAGCAAA	418	3842	UUUGCUAGAGAAGGCAAGG	2170
rs3025843	3825	CUUGCCUUCUCUAGCAAAC	419	3825	CUUGCCUUCUCUAGCAAAC	419	3843	GUUUGCUAGAGAAGGCAAG	2171
rs3025843	3826	UUGCCUUCUCUAGCAAAACC	420	3826	UUGCCUUCUCUAGCAAAACC	420	3844	GGUUUGCUAGAGAAGGCA	2172
rs3025843	3827	UGCCUUCUCUAGCAAAACCC	421	3827	UGCCUUCUCUAGCAAAACCC	421	3845	GGUUUGCUAGAGAAGGC	2173
rs3025843	3828	GCCUUCUCUAGCAAAACCCC	422	3828	GCCUUCUCUAGCAAAACCCC	422	3846	GGGUUUUGCUAGAGAAGGC	2174
rs3025843	3829	CCUUCUCUAGCAAAACCCCC	423	3829	CCUUCUCUAGCAAAACCCCC	423	3847	GGGGUUUUGCUAGAGAAGG	2175
rs3025843	3830	CUUCUCUAGCAAAACCCCCC	424	3830	CUUCUCUAGCAAAACCCCCC	424	3848	GGGGGUUUGCUAGAGAAG	2176
rs3025843	3831	UUCUCUAGCAAAACCCCCCU	425	3831	UUCUCUAGCAAAACCCCCCU	425	3849	AGGGGGUUUUGCUAGAGA	2177

rs3025843	3832	UCUCUAGCAAACCCCCCUU	426	3832	UCUCUAGCAAACCCCCCUU	426	3850	AAGGGGGUUUGCUAGAGA	2178
rs3025843	3833	CUCUAGCAAACCCCCCUUC	427	3833	CUCUAGCAAACCCCCCUUC	427	3851	GAAGGGGGUUUGCUAGAG	2179
rs3025843	3834	UCUAGCAAACCCCCCUUCU	428	3834	UCUAGCAAACCCCCCUUCU	428	3852	AGAAGGGGGUUUGCUAGA	2180
rs3025843	3835	CUAGCAAACCCCCCUUCUC	429	3835	CUAGCAAACCCCCCUUCUC	429	3853	GAGAAGGGGGUUUGCUAG	2181
rs3025843	3836	UAGCAAACCCCCCUUCUCU	430	3836	UAGCAAACCCCCCUUCUCU	430	3854	AGAGAAGGGGGUUUGCUA	2182
rs3025843	3837	AGCAAACCCCCCUUCUCUA	431	3837	AGCAAACCCCCCUUCUCUA	431	3855	UAGAGAAGGGGGUUUGCU	2183
rs3025843	3838	GCAAACCCCCCUUCUCUAA	432	3838	GCAAACCCCCCUUCUCUAA	432	3856	UUAGAGAAGGGGGUUUGC	2184
rs4690074	4104	AAAGUUUGGAGGGUUUCUC	433	4104	AAAGUUUGGAGGGUUUCUC	433	4122	GAGAAACCCUCCAAACUUU	2185
rs4690074	4105	AAGUUUGGAGGGUUUCUCC	434	4105	AAGUUUGGAGGGUUUCUCC	434	4123	GGAGAAACCCUCCAAACUU	2186
rs4690074	4106	AGUUUGGAGGGUUUCUCCG	435	4106	AGUUUGGAGGGUUUCUCCG	435	4124	CGAGAAACCCUCCAAACU	2187
rs4690074	4107	GUUUGGAGGGUUUCUCCGC	436	4107	GUUUGGAGGGUUUCUCCGC	436	4125	CGGAGAAACCCUCCAAAC	2188
rs4690074	4108	UUUGGAGGGUUUCUCCGCU	437	4108	UUUGGAGGGUUUCUCCGCU	437	4126	AGCGAGAAACCCUCCAA	2189
rs4690074	4109	UUGGAGGGUUUCUCCGCU	438	4109	UUGGAGGGUUUCUCCGCU	438	4127	GAGCGAGAAACCCUCCAA	2190
rs4690074	4110	UGGAGGGUUUCUCCGCUCA	439	4110	UGGAGGGUUUCUCCGCUCA	439	4128	UGAGCGGAGAAACCCUCC	2191
rs4690074	4111	GGAGGGUUUCUCCGCUACG	440	4111	GGAGGGUUUCUCCGCUACG	440	4129	CUGAGCGGAGAAACCCUCC	2192
rs4690074	4112	GAGGGUUUCUCCGCUACAG	441	4112	GAGGGUUUCUCCGCUACAG	441	4130	GCUGAGCGGAGAAACCCU	2193
rs4690074	4113	AGGGUUUCUCCGCUACAGC	442	4113	AGGGUUUCUCCGCUACAGC	442	4131	GGCUGAGCGGAGAAACCCU	2194
rs4690074	4114	GGUUUCUCCGCUACAGCCU	443	4114	GGUUUCUCCGCUACAGCCU	443	4132	AGGCUGAGCGGAGAAACCC	2195
rs4690074	4115	GGUUUCUCCGCUACAGCCU	444	4115	GGUUUCUCCGCUACAGCCU	444	4133	AAGGCUGAGCGGAGAAACC	2196
rs4690074	4116	GUUUCUCCGCUACAGCCUUG	445	4116	GUUUCUCCGCUACAGCCUUG	445	4134	CAAGGCUGAGCGGAGAAAC	2197
rs4690074	4117	UUUCUCCGCUACAGCCUUGG	446	4117	UUUCUCCGCUACAGCCUUGG	446	4135	CCAAGGCUGAGCGGAGAA	2198
rs4690074	4118	UUCUCCGCUACAGCCUUGGA	447	4118	UUCUCCGCUACAGCCUUGGA	447	4136	UCCAAGGCUGAGCGGAGAA	2199
rs4690074	4119	UCUCGCUACAGCCUUGGAU	448	4119	UCUCGCUACAGCCUUGGAU	448	4137	AUCCAAGGCUGAGCGGAGA	2200
rs4690074	4120	CUCGCUACAGCCUUGGAUG	449	4120	CUCGCUACAGCCUUGGAUG	449	4138	CAUCCAAGGCUGAGCGGAG	2201
rs4690074	4121	UCCGCUACAGCCUUGGAUGU	450	4121	UCCGCUACAGCCUUGGAUGU	450	4139	ACAUCCAAGGCUGAGCGGA	2202
rs4690074	4122	CCGCUACAGCCUUGGAUGUU	451	4122	CCGCUACAGCCUUGGAUGUU	451	4140	AACAUCCAAGGCUGAGCGG	2203
rs4690074	4104	AAAGUUUGGAGGGUUUCUU	452	4104	AAAGUUUGGAGGGUUUCUU	452	4122	AAGAAACCCUCCAAACUUU	2204
rs4690074	4105	AAGUUUGGAGGGUUUCUUC	453	4105	AAGUUUGGAGGGUUUCUUC	453	4123	GAGAAACCCUCCAAACUU	2205
rs4690074	4106	AGUUUGGAGGGUUUCUUCG	454	4106	AGUUUGGAGGGUUUCUUCG	454	4124	CGAAGAAACCCUCCAAACU	2206
rs4690074	4107	GUUUGGAGGGUUUCUUCGC	455	4107	GUUUGGAGGGUUUCUUCGC	455	4125	GCGAAGAAACCCUCCAAAC	2207
rs4690074	4108	UUUGGAGGGUUUCUUCGCU	456	4108	UUUGGAGGGUUUCUUCGCU	456	4126	AGCGAAGAAACCCUCCAA	2208
rs4690074	4109	UUGGAGGGUUUCUUCGCUC	457	4109	UUGGAGGGUUUCUUCGCUC	457	4127	GAGCGAAGAAACCCUCCAA	2209
rs4690074	4110	UGGAGGGUUUCUUCGCUCA	458	4110	UGGAGGGUUUCUUCGCUCA	458	4128	UGAGCGAAGAAACCCUCCA	2210
rs4690074	4111	GGAGGGUUUCUUCGCUCAG	459	4111	GGAGGGUUUCUUCGCUCAG	459	4129	CUGAGCGAAGAAACCCUCC	2211
rs4690074	4112	GAGGGUUUCUUCGCUCAGC	460	4112	GAGGGUUUCUUCGCUCAGC	460	4130	GCUGAGCGAAGAAACCCUC	2212
rs4690074	4113	AGGGUUUCUUCGCUCAGCC	461	4113	AGGGUUUCUUCGCUCAGCC	461	4131	GGCUGAGCGAAGAAACCCU	2213
rs4690074	4114	GGGUUUCUUCGCUCAGCCU	462	4114	GGGUUUCUUCGCUCAGCCU	462	4132	AGGCUGAGCGAAGAAACCC	2214
rs4690074	4115	GGUUUCUUCGCUCAGCCUU	463	4115	GGUUUCUUCGCUCAGCCUU	463	4133	AAGGCUGAGCGAAGAAACC	2215
rs4690074	4116	GUUUCUUCGCUCAGCCUUG	464	4116	GUUUCUUCGCUCAGCCUUG	464	4134	CAAGGCUGAGCGAAGAAAC	2216

rs4690074	4117	UUUUUCGCUACGCCUUGG	465	4117	UUUUUCGCUACGCCUUGG	465	4135	CCAAAGGUGAGCGAAGAA	2217
rs4690074	4118	UUUUUCGCUACGCCUUGG	466	4118	UUUUUCGCUACGCCUUGG	466	4136	UCCAAGGUGAGCGAAGAA	2218
rs4690074	4119	UUUUUCGCUACGCCUUGG	467	4119	UUUUUCGCUACGCCUUGG	467	4137	AUCCAAGGUGAGCGAAG	2219
rs4690074	4120	UUUUUCGCUACGCCUUGG	468	4120	UUUUUCGCUACGCCUUGG	468	4138	CAUCCAAGGUGAGCGAAG	2220
rs4690074	4121	UUUUUCGCUACGCCUUGG	469	4121	UUUUUCGCUACGCCUUGG	469	4139	ACAUCCAAGGUGAGCGAA	2221
rs4690074	4122	UUUUUCGCUACGCCUUGG	470	4122	UUUUUCGCUACGCCUUGG	470	4140	AACAUCCAAGGUGAGCGA	2222
rs3025837	4456	GUGCAGGCGGAGCAGGAGA	471	4456	GUGCAGGCGGAGCAGGAGA	471	4474	UUCUCCUGCUCCGCCUGC	2223
rs3025837	4457	UGCAGGCGGAGCAGGAGAA	472	4457	UGCAGGCGGAGCAGGAGAA	472	4475	UUCUCCUGCUCCGCCUGCA	2224
rs3025837	4458	GCAGGCGGAGCAGGAGAAC	473	4458	GCAGGCGGAGCAGGAGAAC	473	4476	GUUUCUCCUGCUCCGCCUGC	2225
rs3025837	4459	CAGGCGGAGCAGGAGAAC	474	4459	CAGGCGGAGCAGGAGAAC	474	4477	CGUUCUCCUGCUCCGCCUG	2226
rs3025837	4460	AGGCGGAGCAGGAGAAC	475	4460	AGGCGGAGCAGGAGAAC	475	4478	UCGUUCUCCUGCUCCGCCU	2227
rs3025837	4461	GGCGGAGCAGGAGAAC	476	4461	GGCGGAGCAGGAGAAC	476	4479	GUGUUCUCCUGCUCCGCC	2228
rs3025837	4462	GCGGAGCAGGAGAAC	477	4462	GCGGAGCAGGAGAAC	477	4480	UGUGUUCUCCUGCUCCGCC	2229
rs3025837	4463	CGGAGCAGGAGAAC	478	4463	CGGAGCAGGAGAAC	478	4481	GUGUGUUCUCCUGCUCCGCC	2230
rs3025837	4464	GGAGCAGGAGAAC	479	4464	GGAGCAGGAGAAC	479	4482	GGUGUGUUCUCCUGCUCC	2231
rs3025837	4465	GAGCAGGAGAAC	480	4465	GAGCAGGAGAAC	480	4483	AGGUGUGUUCUCCUGCU	2232
rs3025837	4466	AGCAGGAGAAC	481	4466	AGCAGGAGAAC	481	4484	GAGGUGUGUUCUCCUGCU	2233
rs3025837	4467	GCAGGAGAAC	482	4467	GCAGGAGAAC	482	4485	CGAGGUGUGUUCUCCUGC	2234
rs3025837	4468	CAGGAGAAC	483	4468	CAGGAGAAC	483	4486	CCGAGGUGUGUUCUCCUG	2235
rs3025837	4469	AGGAGAAC	484	4469	AGGAGAAC	484	4487	CCCGAGGUGUGUUCUCCU	2236
rs3025837	4470	GGAGAAC	485	4470	GGAGAAC	485	4488	UCCCGAGGUGUGUUCUCC	2237
rs3025837	4471	GAGAAC	486	4471	GAGAAC	486	4489	AUCCCGAGGUGUGUUCU	2238
rs3025837	4472	AGAAC	487	4472	AGAAC	487	4490	CAUCCCGAGGUGUGUUCU	2239
rs3025837	4473	GAAC	488	4473	GAAC	488	4491	CCAUCGCGAGGUGUGUUC	2240
rs3025837	4474	AAC	489	4474	AAC	489	4492	ACCAUCCGAGGUGUGUUC	2241
rs3025837	4456	GUGCAGGCGGAGCAGGAGC	490	4456	GUGCAGGCGGAGCAGGAGC	490	4474	GCUCUCCUGCUCCGCCUGC	2242
rs3025837	4457	UGCAGGCGGAGCAGGAGCA	491	4457	UGCAGGCGGAGCAGGAGCA	491	4475	UGUCCUCCUGCUCCGCCUG	2243
rs3025837	4458	GCAGGCGGAGCAGGAGCAC	492	4458	GCAGGCGGAGCAGGAGCAC	492	4476	GUGUCCUCCUGCUCCGCCUG	2244
rs3025837	4459	CAGGCGGAGCAGGAGCAC	493	4459	CAGGCGGAGCAGGAGCAC	493	4477	CGUGUCCUCCUGCUCCGCCUG	2245
rs3025837	4460	AGGCGGAGCAGGAGCAC	494	4460	AGGCGGAGCAGGAGCAC	494	4478	UCGUGUCCUCCUGCUCCGCCUG	2246
rs3025837	4461	GGCGGAGCAGGAGCAC	495	4461	GGCGGAGCAGGAGCAC	495	4479	GUCGUGUCCUCCUGCUCCGCC	2247
rs3025837	4462	GCGGAGCAGGAGCAC	496	4462	GCGGAGCAGGAGCAC	496	4480	UGUGUGUCCUCCUGCUCCGCC	2248
rs3025837	4463	CGGAGCAGGAGCAC	497	4463	CGGAGCAGGAGCAC	497	4481	GUGUGUGUCCUCCUGCUCCGCC	2249
rs3025837	4464	GGAGCAGGAGCAC	498	4464	GGAGCAGGAGCAC	498	4482	GGUGUGUCCUCCUGCUCCGCC	2250
rs3025837	4465	GAGCAGGAGCAC	499	4465	GAGCAGGAGCAC	499	4483	AGGUGUGUCCUCCUGCUCCGCC	2251
rs3025837	4466	AGCAGGAGCAC	500	4466	AGCAGGAGCAC	500	4484	GAGGUGUGUCCUCCUGCUCCGCC	2252
rs3025837	4467	GCAGGAGCAC	501	4467	GCAGGAGCAC	501	4485	CGAGGUGUGUCCUCCUGCUCCGCC	2253
rs3025837	4468	CAGGAGCAC	502	4468	CAGGAGCAC	502	4486	CCGAGGUGUGUCCUCCUGCUCCGCC	2254
rs3025837	4469	AGGAGCAC	503	4469	AGGAGCAC	503	4487	CCCAGGUGUGUCCUCCUGCUCCGCC	2255

rs3025837	4470	GGAGCAGCACACCUCCGGGA	504	4470	GGAGCAGCACACCUCCGGGA	504	4488	UCCCGAGGUGUGUGCUCC	2256
rs3025837	4471	GAGCAGCACACCUCCGGGAU	505	4471	GAGCAGCACACCUCCGGGAU	505	4489	AUCCCGAGGUGUGUGCU	2257
rs3025837	4472	AGCAGCACACCUCCGGGAUG	506	4472	AGCAGCACACCUCCGGGAUG	506	4490	CAUCCCGAGGUGUGUGCU	2258
rs3025837	4473	GCAGCACACCUCCGGGAUGG	507	4473	GCAGCACACCUCCGGGAUGG	507	4491	CCAUCCCGAGGUGUGUGC	2259
rs3025837	4474	CACGACACCUCCGGGAUGGU	508	4474	CACGACACCUCCGGGAUGGU	508	4492	ACCAUCCCGAGGUGUGUG	2260
rs363129	4967	UCUUUGUAUUAAAGAGGAAC	509	4967	UCUUUGUAUUAAAGAGGAAC	509	4985	GUUCCUCUUAUAACAAAGA	2261
rs363129	4968	CUUUGUAUUAAAGAGGAACA	510	4968	CUUUGUAUUAAAGAGGAACA	510	4986	UGUCCUCUUAUAACAAAG	2262
rs363129	4969	UUUGUAUUAAAGAGGAACAA	511	4969	UUUGUAUUAAAGAGGAACAA	511	4987	UUUGUCCUCUUAUAACAAA	2263
rs363129	4970	UUGUAUUAAAGAGGAACAAA	512	4970	UUGUAUUAAAGAGGAACAAA	512	4988	UUUGUCCUCUUAUAACAA	2264
rs363129	4971	UGUAUUAAAGAGGAACAAU	513	4971	UGUAUUAAAGAGGAACAAU	513	4989	AUUUGUCCUCUUAUAUAC	2265
rs363129	4972	GUUUUAAGAGGAACAAUUA	514	4972	GUUUUAAGAGGAACAAUUA	514	4990	AUUUGUCCUCUUAUAUAC	2266
rs363129	4973	UAUUUAAGAGGAACAAUUA	515	4973	UAUUUAAGAGGAACAAUUA	515	4991	UAUUUGUCCUCUUAUAU	2267
rs363129	4974	AUUUAAGAGGAACAAUUA	516	4974	AUUUAAGAGGAACAAUUA	516	4992	UUUUUUUGUCCUCUUAU	2268
rs363129	4975	UUUAAGAGGAACAAUUAAG	517	4975	UUUAAGAGGAACAAUUAAG	517	4993	CUUUUUUUUGUCCUCUUA	2269
rs363129	4976	UAAGAGGAACAAUUAAGC	518	4976	UAAGAGGAACAAUUAAGC	518	4994	GCUUUUUUUUGUCCUCUUA	2270
rs363129	4977	AAGAGGAACAAUUAAGCU	519	4977	AAGAGGAACAAUUAAGCU	519	4995	AGCUUUUUUUUGUCCUCU	2271
rs363129	4978	AGAGGAACAAUUAAGCUG	520	4978	AGAGGAACAAUUAAGCUG	520	4996	CAGCUUUUUUUUGUCCUCU	2272
rs363129	4979	GAGGAACAAUUAAGCUGA	521	4979	GAGGAACAAUUAAGCUGA	521	4997	UCAGCUUUUUUUUGUCCUC	2273
rs363129	4980	AGGAACAAUUAAGCUGAU	522	4980	AGGAACAAUUAAGCUGAU	522	4998	AUCAGCUUUUUUUUGUCCU	2274
rs363129	4981	GGACAAUUAAGCUGAUG	523	4981	GGACAAUUAAGCUGAUG	523	4999	CAUCAGCUUUUUUUUGUCC	2275
rs363129	4982	GAACAAUUAAGCUGAUGC	524	4982	GAACAAUUAAGCUGAUGC	524	5000	GCAUCAGCUUUUUUUUGUCC	2276
rs363129	4983	AACAAUUAAGCUGAUGCA	525	4983	AACAAUUAAGCUGAUGCA	525	5001	UGCAUCAGCUUUUUUUUGU	2277
rs363129	4984	ACAAUUAAGCUGAUGCAG	526	4984	ACAAUUAAGCUGAUGCAG	526	5002	CUGCAUCAGCUUUUUUUUG	2278
rs363129	4985	CAAAUUAAGCUGAUGCAGG	527	4985	CAAAUUAAGCUGAUGCAGG	527	5003	CCUGCAUCAGCUUUUUUUUG	2279
rs363129	4967	UCUUUGUAUUAAAGAGGAU	528	4967	UCUUUGUAUUAAAGAGGAU	528	4985	AUUCUCUCUUAUAACAAAGA	2280
rs363129	4968	CUUUGUAUUAAAGAGGAUA	529	4968	CUUUGUAUUAAAGAGGAUA	529	4986	UAUUCUCUCUUAUAACAAAG	2281
rs363129	4969	UUUGUAUUAAAGAGGAUUA	530	4969	UUUGUAUUAAAGAGGAUUA	530	4987	UUAUUCUCUCUUAUAACAAA	2282
rs363129	4970	UUGUAUUAAAGAGGAUAAA	531	4970	UUGUAUUAAAGAGGAUAAA	531	4988	UUUAUUCUCUCUUAUAACAA	2283
rs363129	4971	UGUAUUAAAGAGGAUAAU	532	4971	UGUAUUAAAGAGGAUAAU	532	4989	AUUUAUUCUCUCUUAUAACA	2284
rs363129	4972	GUUUUAAGAGGAUAAUUA	533	4972	GUUUUAAGAGGAUAAUUA	533	4990	UAUUUAUUCUCUCUUAUAAC	2285
rs363129	4973	UAUUUAAGAGGAUAAUUA	534	4973	UAUUUAAGAGGAUAAUUA	534	4991	UUAUUUAUUCUCUCUUAUA	2286
rs363129	4974	AUUUAAGAGGAUAAUUA	535	4974	AUUUAAGAGGAUAAUUA	535	4992	UUUAUUUAUUCUCUCUUAU	2287
rs363129	4975	UUUAAGAGGAUAAUUAAG	536	4975	UUUAAGAGGAUAAUUAAG	536	4993	CUUUUUUUUAUUCUCUUA	2288
rs363129	4976	UUAAGAGGAUAAUUAAGC	537	4976	UUAAGAGGAUAAUUAAGC	537	4994	GCUUUUUUUUAUUCUCUUA	2289
rs363129	4977	AAGAGGAUAAUUAAGCU	538	4977	AAGAGGAUAAUUAAGCU	538	4995	AGCUUUUUUUUAUUCUCU	2290
rs363129	4978	AGAGGAUAAUUAAGCUG	539	4978	AGAGGAUAAUUAAGCUG	539	4996	CAGCUUUUUUUUAUUCUCU	2291
rs363129	4979	GAGGAUAAUUAAGCUGA	540	4979	GAGGAUAAUUAAGCUGA	540	4997	UCAGCUUUUUUUUAUUCUC	2292
rs363129	4980	AGGAUAAUUAAGCUGAU	541	4980	AGGAUAAUUAAGCUGAU	541	4998	AUCAGCUUUUUUUUAUUCU	2293
rs363129	4981	GGAUAAUUAAGCUGAUG	542	4981	GGAUAAUUAAGCUGAUG	542	4999	CAUCAGCUUUUUUUUAUUC	2294

rs363129	4982	GAAUAAUAAAGCUGAUGC	543	4982	GAAUAAUAAAGCUGAUGC	543	5000	GCAUCAGCUUUUUUUUUC	2295
rs363129	4983	AUAAUAAAGCUGAUGC	544	4983	AUAAUAAAGCUGAUGC	544	5001	UGCAUCAGCUUUUUUUUU	2296
rs363129	4984	AUAAUAAAGCUGAUGC	545	4984	AUAAUAAAGCUGAUGC	545	5002	CUGCAUCAGCUUUUUUUU	2297
rs363129	4985	UAAUAAAGCUGAUGC	546	4985	UAAUAAAGCUGAUGC	546	5003	CCUGCAUCAGCUUUUUUA	2298
rs363125	5462	UAAGAGUUGGGACAGUAC	547	5462	UAAGAGUUGGGACAGUAC	547	5480	GUACUGUCCCCAUCUCUA	2299
rs363125	5463	AAGAGUUGGGACAGUACU	548	5463	AAGAGUUGGGACAGUACU	548	5481	AGUACUGUCCCCAUCUCU	2300
rs363125	5464	AGAGUUGGGACAGUACUU	549	5464	AGAGUUGGGACAGUACUU	549	5482	AAGUACUGUCCCCAUCUCU	2301
rs363125	5465	GAGUUGGGACAGUACUUC	550	5465	GAGUUGGGACAGUACUUC	550	5483	GAGUACUGUCCCCAUCUC	2302
rs363125	5466	AGAUGGGACAGUACUUA	551	5466	AGAUGGGACAGUACUUA	551	5484	UGAAGUACUGUCCCCAUCU	2303
rs363125	5467	GAUGGGACAGUACUCAA	552	5467	GAUGGGACAGUACUCAA	552	5485	UUGAAGUACUGUCCCCAUC	2304
rs363125	5468	AUGGGACAGUACUUAAC	553	5468	AUGGGACAGUACUUAAC	553	5486	GUUGAAGUACUGUCCCCCAU	2305
rs363125	5469	UGGGACAGUACUUAACG	554	5469	UGGGACAGUACUUAACG	554	5487	CGUUGAAGUACUGUCCCCA	2306
rs363125	5470	GGGACAGUACUUAACGC	555	5470	GGGACAGUACUUAACGC	555	5488	GCGUUGAAGUACUGUCCCC	2307
rs363125	5471	GGGACAGUACUUAACGCU	556	5471	GGGACAGUACUUAACGCU	556	5489	AGCGUUGAAGUACUGUCCC	2308
rs363125	5472	GGACAGUACUUAACGCUA	557	5472	GGACAGUACUUAACGCUA	557	5490	UAGCGUUGAAGUACUGUCC	2309
rs363125	5473	GACAGUACUUAACGCUAG	558	5473	GACAGUACUUAACGCUAG	558	5491	CUAGCGUUGAAGUACUGUC	2310
rs363125	5474	ACAGUACUUAACGCUAGA	559	5474	ACAGUACUUAACGCUAGA	559	5492	UCUAGCGUUGAAGUACUGU	2311
rs363125	5475	CAGUACUUAACGCUAGAA	560	5475	CAGUACUUAACGCUAGAA	560	5493	UUCUAGCGUUGAAGUACUG	2312
rs363125	5476	AGUACUUAACGCUAGAAG	561	5476	AGUACUUAACGCUAGAAG	561	5494	CUUCUAGCGUUGAAGUACU	2313
rs363125	5477	GUACUUAACGCUAGAAGA	562	5477	GUACUUAACGCUAGAAGA	562	5495	UCUUCUAGCGUUGAAGUAC	2314
rs363125	5478	UACUUAACGCUAGAAGAA	563	5478	UACUUAACGCUAGAAGAA	563	5496	UUCUUCUAGCGUUGAAGUA	2315
rs363125	5479	ACUUAACGCUAGAAGAAC	564	5479	ACUUAACGCUAGAAGAAC	564	5497	GUUCUUCUAGCGUUGAAGU	2316
rs363125	5480	CUUCAACGCUAGAAGAAC	565	5480	CUUCAACGCUAGAAGAAC	565	5498	UGUUCUUCUAGCGUUGAAG	2317
rs363125	5462	UAAGAGUUGGGACAGUAA	566	5462	UAAGAGUUGGGACAGUAA	566	5480	UUACUGUCCCCAUCUCUUA	2318
rs363125	5463	AAGAGUUGGGACAGUAAU	567	5463	AAGAGUUGGGACAGUAAU	567	5481	AUUACUGUCCCCAUCUCUU	2319
rs363125	5464	AGAGUUGGGACAGUAAUU	568	5464	AGAGUUGGGACAGUAAUU	568	5482	AAUUACUGUCCCCAUCUCU	2320
rs363125	5465	GAGUUGGGACAGUAAUUC	569	5465	GAGUUGGGACAGUAAUUC	569	5483	GAAUUCUGUCCCCAUCUC	2321
rs363125	5466	AGAUGGGACAGUAAUUA	570	5466	AGAUGGGACAGUAAUUA	570	5484	UGAAUUCUGUCCCCAUCU	2322
rs363125	5467	AUGGGGACAGUAAUCAA	571	5467	AUGGGGACAGUAAUCAA	571	5485	UUGAAUUCUGUCCCCCAUC	2323
rs363125	5468	AUGGGACAGUAAUUAAC	572	5468	AUGGGACAGUAAUUAAC	572	5486	GUUGAAUUCUGUCCCCCAU	2324
rs363125	5469	UGGGACAGUAAUUAACG	573	5469	UGGGACAGUAAUUAACG	573	5487	GUGUAAUUCUGUCCCCCA	2325
rs363125	5470	GGGACAGUAAUUAACGC	574	5470	GGGACAGUAAUUAACGC	574	5488	GCGUUGAAUUCUGUCCCC	2326
rs363125	5471	GGGACAGUAAUUAACGCU	575	5471	GGGACAGUAAUUAACGCU	575	5489	AGCGUUGAAUUCUGUCCCC	2327
rs363125	5472	GGACAGUAAUUAACGCUA	576	5472	GGACAGUAAUUAACGCUA	576	5490	UAGCGUUGAAUUCUGUCC	2328
rs363125	5473	GACAGUAAUUAACGCUAG	577	5473	GACAGUAAUUAACGCUAG	577	5491	CUAGCGUUGAAUUCUGUC	2329
rs363125	5474	ACAGUAAUUAACGCUAGA	578	5474	ACAGUAAUUAACGCUAGA	578	5492	UCUAGCGUUGAAUUCUGU	2330
rs363125	5475	CAGUAAUUAACGCUAGAA	579	5475	CAGUAAUUAACGCUAGAA	579	5493	UUCUAGCGUUGAAUUCUG	2331
rs363125	5476	AGUAAUUAACGCUAGAA	580	5476	AGUAAUUAACGCUAGAA	580	5494	CUUCUAGCGUUGAAUUCU	2332
rs363125	5477	GUAAUUAACGCUAGAA	581	5477	GUAAUUAACGCUAGAA	581	5495	UCUUCUAGCGUUGAAUUC	2333

rs363125	5478	UAAUUAACGCUAGAAGAA	582	5478	UAAUUAACGCUAGAAGAA	582	5496	UUUUUUUAGCGUUGAAUUA	2334
rs363125	5479	AUUUAACGCUAGAAGAAC	583	5479	AUUUAACGCUAGAAGAAC	583	5497	GUUUUUUAGCGUUGAAUU	2335
rs363125	5480	AUUUAACGCUAGAAGAAC	584	5480	AUUUAACGCUAGAAGAAC	584	5498	UGUUUUUAGCGUUGAAU	2336
rs4690077	6894	GCCCGAGCUGCCUGCAGAG	585	6894	GCCCGAGCUGCCUGCAGAG	585	6912	CUCUGCAGGCGCUCGGGC	2337
rs4690077	6895	CCCGAGCUGCCUGCAGAGC	586	6895	CCCGAGCUGCCUGCAGAGC	586	6913	GCUCUGCAGGCGCUCGGG	2338
rs4690077	6896	CCGAGCUGCCUGCAGAGCC	587	6896	CCGAGCUGCCUGCAGAGCC	587	6914	GGCUCUGCAGGCGCUCGG	2339
rs4690077	6897	CGAGCUGCCUGCAGAGCCG	588	6897	CGAGCUGCCUGCAGAGCCG	588	6915	CGGCUUGCAGGCGCUCUG	2340
rs4690077	6898	GAGCUGCCUGCAGAGCCGG	589	6898	GAGCUGCCUGCAGAGCCGG	589	6916	CCGGCUCUGCAGGCGCUC	2341
rs4690077	6899	AGCUGCCUGCAGAGCCGGC	590	6899	AGCUGCCUGCAGAGCCGGC	590	6917	GCCGGCUCUGCAGGCGCU	2342
rs4690077	6900	GUUCCUGCAGAGCCGGCG	591	6900	GUUCCUGCAGAGCCGGCG	591	6918	CGCCGGCUCUGCAGGCGC	2343
rs4690077	6901	CUGCCUGCAGAGCCGGCGG	592	6901	CUGCCUGCAGAGCCGGCGG	592	6919	CGCCGGCUCUGCAGGCGC	2344
rs4690077	6902	UGCCUGCAGAGCCGGCGGC	593	6902	UGCCUGCAGAGCCGGCGGC	593	6920	GCCGCGGCUUGCAGGCA	2345
rs4690077	6903	GCCUGCAGAGCCGGCGGCC	594	6903	GCCUGCAGAGCCGGCGGCC	594	6921	GGCCGCGGCUUGCAGGCG	2346
rs4690077	6904	CCUGCAGAGCCGGCGGCCU	595	6904	CCUGCAGAGCCGGCGGCCU	595	6922	AGGCGCGGCGCUCUGCAG	2347
rs4690077	6905	CUGCAGAGCCGGCGGCCUA	596	6905	CUGCAGAGCCGGCGGCCUA	596	6923	UAGGCGCGGCGCUCUGCAG	2348
rs4690077	6906	UGCAGAGCCGGCGGCCUAC	597	6906	UGCAGAGCCGGCGGCCUAC	597	6924	GUAGGCGCGGCGCUCUGCA	2349
rs4690077	6907	GCAGAGCCGGCGGCCUACU	598	6907	GCAGAGCCGGCGGCCUACU	598	6925	AGUAGGCGCGGCGCUCUGC	2350
rs4690077	6908	CAGAGCCGGCGGCCUACUG	599	6908	CAGAGCCGGCGGCCUACUG	599	6926	CAGUAGGCGCGGCGCUCUG	2351
rs4690077	6909	AGAGCCGGCGGCCUACUGG	600	6909	AGAGCCGGCGGCCUACUGG	600	6927	CCAGUAGGCGCGGCGCUCU	2352
rs4690077	6910	GAGCCGGCGGCCUACUGGA	601	6910	GAGCCGGCGGCCUACUGGA	601	6928	UCCAGUAGGCGCGGCGCUC	2353
rs4690077	6911	AGCCGGCGGCCUACUGGAG	602	6911	AGCCGGCGGCCUACUGGAG	602	6929	CUCCAGUAGGCGCGGCGCUC	2354
rs4690077	6912	GCCGGCGGCCUACUGGAGC	603	6912	GCCGGCGGCCUACUGGAGC	603	6930	GCUCAGUAGGCGCGGCGGC	2355
rs4690077	6894	GCCGAGCUGCCUGCAGAA	604	6894	GCCGAGCUGCCUGCAGAA	604	6912	UUUCUGCAGGCGCUCGGGC	2356
rs4690077	6895	CCGAGCUGCCUGCAGAAC	605	6895	CCGAGCUGCCUGCAGAAC	605	6913	GUUCUGCAGGCGCUCGGG	2357
rs4690077	6896	CCGAGCUGCCUGCAGAAC	606	6896	CCGAGCUGCCUGCAGAAC	606	6914	GGUUCUGCAGGCGCUCGG	2358
rs4690077	6897	CGAGCUGCCUGCAGAACCG	607	6897	CGAGCUGCCUGCAGAACCG	607	6915	CGGUUCUGCAGGCGCUCG	2359
rs4690077	6898	GAGCUGCCUGCAGAACCCG	608	6898	GAGCUGCCUGCAGAACCCG	608	6916	CCGGUUCUGCAGGCGCUC	2360
rs4690077	6899	AGCUGCCUGCAGAACCCGC	609	6899	AGCUGCCUGCAGAACCCGC	609	6917	GCCGUUCUGCAGGCGCUC	2361
rs4690077	6900	GCUGCCUGCAGAACCCGGCG	610	6900	GCUGCCUGCAGAACCCGGCG	610	6918	CGCCGGUUCUGCAGGCGC	2362
rs4690077	6901	CUGCCUGCAGAACCCGGCGG	611	6901	CUGCCUGCAGAACCCGGCGG	611	6919	CGCCGGUUCUGCAGGCGC	2363
rs4690077	6902	UGCCUGCAGAACCCGGCGGC	612	6902	UGCCUGCAGAACCCGGCGGC	612	6920	GCCGCGGCUUCUGCAGGCA	2364
rs4690077	6903	GCCUGCAGAACCCGGCGGCC	613	6903	GCCUGCAGAACCCGGCGGCC	613	6921	GGCCGCGGCUUCUGCAGGC	2365
rs4690077	6904	CCUGCAGAACCCGGCGGCCU	614	6904	CCUGCAGAACCCGGCGGCCU	614	6922	AGGCGCGGCUUCUGCAGG	2366
rs4690077	6905	CUGCAGAACCCGGCGGCCUA	615	6905	CUGCAGAACCCGGCGGCCUA	615	6923	UAGGCGCGGCUUCUGCAG	2367
rs4690077	6906	UGCAGAACCCGGCGGCCUAC	616	6906	UGCAGAACCCGGCGGCCUAC	616	6924	GUAGGCGCGGCUUCUGCA	2368
rs4690077	6907	GCAGAACCCGGCGGCCUACU	617	6907	GCAGAACCCGGCGGCCUACU	617	6925	AGUAGGCGCGGCUUCUGC	2369
rs4690077	6908	CAGAACCCGGCGGCCUACUG	618	6908	CAGAACCCGGCGGCCUACUG	618	6926	CAGUAGGCGCGGCUUCUG	2370
rs4690077	6909	AGAACCCGGCGGCCUACUGG	619	6909	AGAACCCGGCGGCCUACUGG	619	6927	CCAGUAGGCGCGGCUUCU	2371
rs4690077	6910	GAACCGCGGCCUACUGGA	620	6910	GAACCGCGGCCUACUGGA	620	6928	UCCAGUAGGCGCGGCUUC	2372

rs4690077	6911	AACGGGGCCUACUGGAG	621	6911	AACGGGGCCUACUGGAG	621	6929	CUCCAGUAGGCCGCCGGU	2373
rs4690077	6912	ACGGGGCCUACUGGAGC	622	6912	ACGGGGCCUACUGGAGC	622	6930	GUCCAGUAGGCCGCCGGU	2374
rs362331	7228	CAGCCUGCUCUCCUACU	623	7228	CAGCCUGCUCUCCUACU	623	7246	AGAUGAGGAGCAGGCCGUG	2375
rs362331	7229	ACGCCUGCUCUCCUACUA	624	7229	ACGCCUGCUCUCCUACUA	624	7247	UAGAUGAGGAGCAGGCCGUG	2376
rs362331	7230	CGCCUGCUCUCCUACUAC	625	7230	CGCCUGCUCUCCUACUAC	625	7248	GUAGAUGAGGAGCAGGCCG	2377
rs362331	7231	GCCUGCUCUCCUACUACU	626	7231	GCCUGCUCUCCUACUACU	626	7249	AGUAGAUGAGGAGCAGGC	2378
rs362331	7232	CCUGCUCUCCUACUACUG	627	7232	CCUGCUCUCCUACUACUG	627	7250	CAGUAGAUGAGGAGCAGG	2379
rs362331	7233	CUGCUCUCCUACUACUGU	628	7233	CUGCUCUCCUACUACUGU	628	7251	ACAGUAGAUGAGGAGCAG	2380
rs362331	7234	UGCUCUCCUACUACUGUG	629	7234	UGCUCUCCUACUACUGUG	629	7252	CACAGUAGAUGAGGAGCA	2381
rs362331	7235	GUCCUACUACUACUGUGU	630	7235	GUCCUACUACUACUGUGU	630	7253	ACACAGUAGAUGAGGGAGC	2382
rs362331	7236	CUCCUACUACUACUGUGU	631	7236	CUCCUACUACUACUGUGU	631	7254	CACACAGUAGAUGGGGAG	2383
rs362331	7237	UCCUACUACUACUGUGGC	632	7237	UCCUACUACUACUGUGGC	632	7255	GCACACAGUAGAUGAGGGA	2384
rs362331	7238	CCCUACUACUACUGUGCA	633	7238	CCCUACUACUACUGUGCA	633	7256	UGCACACAGUAGAUGAGGG	2385
rs362331	7239	CCUACUACUACUGUGGCAC	634	7239	CCUACUACUACUGUGGCAC	634	7257	GUGCACACAGUAGAUGAGG	2386
rs362331	7240	CUCAUCUACUGUGGCACU	635	7240	CUCAUCUACUGUGGCACU	635	7258	AGUGCACACAGUAGAUGAG	2387
rs362331	7241	UCAUCUACUGUGGCACUU	636	7241	UCAUCUACUGUGGCACUU	636	7259	AAGUGCACACAGUAGAUGA	2388
rs362331	7242	CAUCUACUGUGGCACUUC	637	7242	CAUCUACUGUGGCACUUC	637	7260	GAAGUGCACACAGUAGAUG	2389
rs362331	7243	AUCUACUGUGGCACUUA	638	7243	AUCUACUGUGGCACUUA	638	7261	UGAAGUGCACACAGUAGA	2390
rs362331	7244	UCUACUGUGGCACUUAU	639	7244	UCUACUGUGGCACUUAU	639	7262	AUGAAGUGCACACAGUAGA	2391
rs362331	7245	CUACUGUGGCACUUAUC	640	7245	CUACUGUGGCACUUAUC	640	7263	GAUGAAGUGCACACAGUAG	2392
rs362331	7246	UACUGUGGCACUUAUCC	641	7246	UACUGUGGCACUUAUCC	641	7264	GGAUGAGGAGCAGGCCGUG	2393
rs362331	7228	CAGCCUGCUCUCCUACUCC	642	7228	CAGCCUGCUCUCCUACUCC	642	7246	GGAUGAGGAGCAGGCCGUG	2394
rs362331	7229	ACGCCUGCUCUCCUACUCCA	643	7229	ACGCCUGCUCUCCUACUCCA	643	7247	UGGAUGAGGAGCAGGCCGUG	2395
rs362331	7230	CGCCUGCUCUCCUACUCCAC	644	7230	CGCCUGCUCUCCUACUCCAC	644	7248	GUGGAUGAGGAGCAGGCCG	2396
rs362331	7231	GCCUGCUCUCCUACUCCACU	645	7231	GCCUGCUCUCCUACUCCACU	645	7249	AGUGGAUGAGGAGCAGGCC	2397
rs362331	7232	CCUGCUCUCCUACUCCACUG	646	7232	CCUGCUCUCCUACUCCACUG	646	7250	CAGUGGAUGAGGAGCAGG	2398
rs362331	7233	CUGCUCUCCUACUCCACUGU	647	7233	CUGCUCUCCUACUCCACUGU	647	7251	ACAGUGGAUGAGGAGCAG	2399
rs362331	7234	UGCUCUCCUACUCCACUGUG	648	7234	UGCUCUCCUACUCCACUGUG	648	7252	CACAGUGGAUGAGGAGCA	2400
rs362331	7235	GCUCUCCUACUCCACUGUGU	649	7235	GCUCUCCUACUCCACUGUGU	649	7253	ACACAGUGGAUGAGGAGC	2401
rs362331	7236	CUCCUACUCCACUGUGUG	650	7236	CUCCUACUCCACUGUGUG	650	7254	CACACAGUGGAUGAGGAG	2402
rs362331	7237	UCCCUACUCCACUGUGUGC	651	7237	UCCCUACUCCACUGUGUGC	651	7255	GCACACAGUGGAUGAGGGA	2403
rs362331	7238	CCCUACUCCACUGUGUGCA	652	7238	CCCUACUCCACUGUGUGCA	652	7256	UGCACACAGUGGAUGAGGG	2404
rs362331	7239	CCUACUCCACUGUGUGCAC	653	7239	CCUACUCCACUGUGUGCAC	653	7257	GUGCACACAGUGGAUGAGG	2405
rs362331	7240	CUCAUCCACUGUGUGCACU	654	7240	CUCAUCCACUGUGUGCACU	654	7258	AGUGCACACAGUGGAUGAG	2406
rs362331	7241	UCAUCCACUGUGUGCACUU	655	7241	UCAUCCACUGUGUGCACUU	655	7259	AAGUGCACACAGUGGAUGA	2407
rs362331	7242	CAUCCACUGUGUGCACUUC	656	7242	CAUCCACUGUGUGCACUUC	656	7260	GAAGUGCACACAGUGGAUG	2408
rs362331	7243	AUCCACUGUGUGCACUUA	657	7243	AUCCACUGUGUGCACUUA	657	7261	UGAAGUGCACACAGUGGAU	2409
rs362331	7244	UCCACUGUGUGCACUUAU	658	7244	UCCACUGUGUGCACUUAU	658	7262	AUGAAGUGCACACAGUGGA	2410
rs362331	7245	CCACUGUGUGCACUUAUC	659	7245	CCACUGUGUGCACUUAUC	659	7263	GAUGAAGUGCACACAGUGG	2411

rs362331	7246	CACUGUGGCACUUAUCC	660	7246	CACUGUGGCACUUAUCC	660	7264	GGAUGAAGUGCACACAGUG	2412
rs3025818	7365	AAACACACAGAAUCCUAAG	661	7365	AAACACACAGAAUCCUAAG	661	7383	CUUAGGAUUCUGUGUGUUU	2413
rs3025818	7366	AACACACAGAAUCCUAAGU	662	7366	AACACACAGAAUCCUAAGU	662	7384	ACUUAGGAUUCUGUGUGUU	2414
rs3025818	7367	ACACACAGAAUCCUAAGUA	663	7367	ACACACAGAAUCCUAAGUA	663	7385	UACUUAGGAUUCUGUGUGU	2415
rs3025818	7368	CACACAGAAUCCUAAGUAU	664	7368	CACACAGAAUCCUAAGUAU	664	7386	AUACUUAGGAUUCUGUGUG	2416
rs3025818	7369	ACACAGAAUCCUAAGUAUA	665	7369	ACACAGAAUCCUAAGUAUA	665	7387	UAUACUUAGGAUUCUGUGU	2417
rs3025818	7370	CACAGAAUCCUAAGUAUAU	666	7370	CACAGAAUCCUAAGUAUAU	666	7388	AUAUACUUAGGAUUCUGUG	2418
rs3025818	7371	ACAGAAUCCUAAGUAUAUC	667	7371	ACAGAAUCCUAAGUAUAUC	667	7389	GAUAUACUUAGGAUUCUGU	2419
rs3025818	7372	CAGAAUCCUAAGUAUAUCA	668	7372	CAGAAUCCUAAGUAUAUCA	668	7390	UGAUUAUACUUAGGAUUCUG	2420
rs3025818	7373	AGAAUCCUAAGUAUAUCAC	669	7373	AGAAUCCUAAGUAUAUCAC	669	7391	GUGAUUAUACUUAGGAUUCU	2421
rs3025818	7374	GAAUCCUAAGUAUAUCACU	670	7374	GAAUCCUAAGUAUAUCACU	670	7392	AGUGAUUAUACUUAGGAUUC	2422
rs3025818	7375	AUCCUAAGUAUAUCACUG	671	7375	AUCCUAAGUAUAUCACUG	671	7393	CAGUGAUUAUACUUAGGAUU	2423
rs3025818	7376	AUCCUAAGUAUAUCACUGC	672	7376	AUCCUAAGUAUAUCACUGC	672	7394	GCAGUGAUUAUACUUAGGAU	2424
rs3025818	7377	UCCUAAGUAUAUCACUGCA	673	7377	UCCUAAGUAUAUCACUGCA	673	7395	UGCAGUGAUUAUACUUAGGA	2425
rs3025818	7378	CCUAAGUAUAUCACUGCAG	674	7378	CCUAAGUAUAUCACUGCAG	674	7396	CUGCAGUGAUUAUACUUAGG	2426
rs3025818	7379	CUAAGUAUAUCACUGCAGC	675	7379	CUAAGUAUAUCACUGCAGC	675	7397	GCUGCAGUGAUUAUACUUAG	2427
rs3025818	7380	UAAGUAUAUCACUGCAGCC	676	7380	UAAGUAUAUCACUGCAGCC	676	7398	GGCUGCAGUGAUUAUACUUA	2428
rs3025818	7381	AAGUAUAUCACUGCAGCCU	677	7381	AAGUAUAUCACUGCAGCCU	677	7399	AGGCUGCAGUGAUUAUACUU	2429
rs3025818	7382	AGUAUAUCACUGCAGCCUG	678	7382	AGUAUAUCACUGCAGCCUG	678	7400	CAGGCUGCAGUGAUUAUACU	2430
rs3025818	7383	GUUAUAUCACUGCAGCCUGU	679	7383	GUUAUAUCACUGCAGCCUGU	679	7401	ACAGGCUGCAGUGAUUAUAC	2431
rs3025818	7365	AAACACACAGAAUCCUAAA	680	7365	AAACACACAGAAUCCUAAA	680	7383	UUUAGGAUUCUGUGUGUUU	2432
rs3025818	7366	AACACACAGAAUCCUAAA	681	7366	AACACACAGAAUCCUAAA	681	7384	AUUUAGGAUUCUGUGUGUU	2433
rs3025818	7367	ACACACAGAAUCCUAAAUA	682	7367	ACACACAGAAUCCUAAAUA	682	7385	UAUUUAGGAUUCUGUGUGU	2434
rs3025818	7368	CACACAGAAUCCUAAAUAU	683	7368	CACACAGAAUCCUAAAUAU	683	7386	AUAUUUAGGAUUCUGUGUG	2435
rs3025818	7369	ACACAGAAUCCUAAAUAUA	684	7369	ACACAGAAUCCUAAAUAUA	684	7387	UAUAUUUAGGAUUCUGUGU	2436
rs3025818	7370	CACAGAAUCCUAAAUAUAU	685	7370	CACAGAAUCCUAAAUAUAU	685	7388	AUAUAUUUAGGAUUCUGUG	2437
rs3025818	7371	ACAGAAUCCUAAAUAUAUC	686	7371	ACAGAAUCCUAAAUAUAUC	686	7389	GAUAUAUUUAGGAUUCUGU	2438
rs3025818	7372	CAGAAUCCUAAAUAUAUCA	687	7372	CAGAAUCCUAAAUAUAUCA	687	7390	UGAUUAUUUAGGAUUCUGU	2439
rs3025818	7373	AGAAUCCUAAAUAUAUCAC	688	7373	AGAAUCCUAAAUAUAUCAC	688	7391	GUGAUUAUUUAGGAUUCU	2440
rs3025818	7374	GAAUCCUAAAUAUAUCACU	689	7374	GAAUCCUAAAUAUAUCACU	689	7392	AGUGAUUAUUUAGGAUUC	2441
rs3025818	7375	AUCCUAAAUAUAUCACUG	690	7375	AUCCUAAAUAUAUCACUG	690	7393	CAGUGAUUAUUUAGGAUU	2442
rs3025818	7376	AUCCUAAAUAUAUCACUGC	691	7376	AUCCUAAAUAUAUCACUGC	691	7394	GCAGUGAUUAUUUAGGAU	2443
rs3025818	7377	UCCUAAAUAUAUCACUGCA	692	7377	UCCUAAAUAUAUCACUGCA	692	7395	UGCAGUGAUUAUUUAGGA	2444
rs3025818	7378	CCUAAAUAUAUCACUGCAG	693	7378	CCUAAAUAUAUCACUGCAG	693	7396	CUGCAGUGAUUAUUUAGG	2445
rs3025818	7379	CUAAAUAUAUCACUGCAGC	694	7379	CUAAAUAUAUCACUGCAGC	694	7397	GCUGCAGUGAUUAUUUAG	2446
rs3025818	7380	UAAAUAUAUCACUGCAGCC	695	7380	UAAAUAUAUCACUGCAGCC	695	7398	GGCUGCAGUGAUUAUUUA	2447
rs3025818	7381	AAUAUAUCACUGCAGCCU	696	7381	AAUAUAUCACUGCAGCCU	696	7399	AGGCUGCAGUGAUUAUUU	2448
rs3025818	7382	AUAUAUCACUGCAGCCUG	697	7382	AUAUAUCACUGCAGCCUG	697	7400	CAGGCUGCAGUGAUUAUU	2449
rs3025818	7383	AUAUAUCACUGCAGCCUGU	698	7383	AUAUAUCACUGCAGCCUGU	698	7401	ACAGGCUGCAGUGAUUAU	2450

rs2857790	7479	GUUUCUCACGCCCAUUGCUC	699	7479	GUUUCUCACGCCCAUUGCUC	699	7497	GAGCAUUGGCGUGAGAAAC	2451
rs2857790	7480	UUUCUCACGCCCAUUGCUC	700	7480	UUUCUCACGCCCAUUGCUC	700	7498	UGAGCAUUGGCGUGAGAAA	2452
rs2857790	7481	UUUCUCACGCCCAUUGCUC	701	7481	UUUCUCACGCCCAUUGCUC	701	7499	CUGAGCAUUGGCGUGAGAA	2453
rs2857790	7482	UCUCACGCCCAUUGCUCAGG	702	7482	UCUCACGCCCAUUGCUCAGG	702	7500	CCUGAGCAUUGGCGUGAGA	2454
rs2857790	7483	CUCACGCCCAUUGCUCAGGA	703	7483	CUCACGCCCAUUGCUCAGGA	703	7501	UCCUGAGCAUUGGCGUGAG	2455
rs2857790	7484	UCACGCCCAUUGCUCAGGAA	704	7484	UCACGCCCAUUGCUCAGGAA	704	7502	UUCUGAGCAUUGGCGUGA	2456
rs2857790	7485	CACGCCCAUUGCUCAGGAAC	705	7485	CACGCCCAUUGCUCAGGAAC	705	7503	GUUCCUGAGCAUUGGCGUG	2457
rs2857790	7486	ACGCCCAUUGCUCAGGAACA	706	7486	ACGCCCAUUGCUCAGGAACA	706	7504	UGUCCUGAGCAUUGGCGU	2458
rs2857790	7487	CGCCCAUUGCUCAGGAACAU	707	7487	CGCCCAUUGCUCAGGAACAU	707	7505	AUGUCCUGAGCAUUGGCG	2459
rs2857790	7488	GCCAUUGCUCAGGAACAUC	708	7488	GCCAUUGCUCAGGAACAUC	708	7506	GAUGUCCUGAGCAUUGGC	2460
rs2857790	7489	CCAUUGCUCAGGAACAUC	709	7489	CCAUUGCUCAGGAACAUC	709	7507	UGAUUCCUGAGCAUUGG	2461
rs2857790	7490	CAUUGCUCAGGAACAUC	710	7490	CAUUGCUCAGGAACAUC	710	7508	AUGAUUCCUGAGCAUUG	2462
rs2857790	7491	AUUGCUCAGGAACAUC	711	7491	AUUGCUCAGGAACAUC	711	7509	GAUGAUUCCUGAGCAU	2463
rs2857790	7492	UUGCUCAGGAACAUC	712	7492	UUGCUCAGGAACAUC	712	7510	UGAUGAUUCCUGAGCAA	2464
rs2857790	7493	UGCUCAGGAACAUC	713	7493	UGCUCAGGAACAUC	713	7511	AUGAUGAUUCCUGAGCA	2465
rs2857790	7494	GCUCAGGAACAUC	714	7494	GCUCAGGAACAUC	714	7512	GAUGAUGAUUCCUGAGC	2466
rs2857790	7495	CUCAGGAACAUC	715	7495	CUCAGGAACAUC	715	7513	UGAUGAUGAUUCCUGAG	2467
rs2857790	7496	UCAGGAACAUC	716	7496	UCAGGAACAUC	716	7514	CUGAUGAUGAUUCCUGA	2468
rs2857790	7497	CAGGAACAUC	717	7497	CAGGAACAUC	717	7515	GCUGAUGAUGAUUCCUG	2469
rs2857790	7479	GUUUCUCACGCCCAUUGCUC	718	7479	GUUUCUCACGCCCAUUGCUC	718	7497	UAGCAUUGGCGUGAGAAA	2470
rs2857790	7480	UUUCUCACGCCCAUUGCUC	719	7480	UUUCUCACGCCCAUUGCUC	719	7498	UUAGCAUUGGCGUGAGAAA	2471
rs2857790	7481	UUUCUCACGCCCAUUGCUC	720	7481	UUUCUCACGCCCAUUGCUC	720	7499	CUUAGCAUUGGCGUGAGAA	2472
rs2857790	7482	UCUCACGCCCAUUGCUC	721	7482	UCUCACGCCCAUUGCUC	721	7500	CCUAGCAUUGGCGUGAGA	2473
rs2857790	7483	CUCACGCCCAUUGCUC	722	7483	CUCACGCCCAUUGCUC	722	7501	UCCUAGCAUUGGCGUGAG	2474
rs2857790	7484	UCACGCCCAUUGCUC	723	7484	UCACGCCCAUUGCUC	723	7502	UUCUAGCAUUGGCGUGA	2475
rs2857790	7485	CACGCCCAUUGCUC	724	7485	CACGCCCAUUGCUC	724	7503	GUUCCUAGCAUUGGCGUG	2476
rs2857790	7486	ACGCCCAUUGCUC	725	7486	ACGCCCAUUGCUC	725	7504	UGUCCUAGCAUUGGCGU	2477
rs2857790	7487	CGCCCAUUGCUC	726	7487	CGCCCAUUGCUC	726	7505	AUGUCCUAGCAUUGGCG	2478
rs2857790	7488	GCCAUUGCUC	727	7488	GCCAUUGCUC	727	7506	GAUGUCCUAGCAUUGGC	2479
rs2857790	7489	CCAUUGCUC	728	7489	CCAUUGCUC	728	7507	UGAUGUCCUAGCAUUGG	2480
rs2857790	7490	CAUUGCUC	729	7490	CAUUGCUC	729	7508	AUGAUGUCCUAGCAUUG	2481
rs2857790	7491	AUUGCUC	730	7491	AUUGCUC	730	7509	GAUGAUGUCCUAGCAU	2482
rs2857790	7492	UUGCUC	731	7492	UUGCUC	731	7510	UGAUGAUGUCCUAGCAA	2483
rs2857790	7493	UGCUAAGGAACAUC	732	7493	UGCUAAGGAACAUC	732	7511	AUGAUGAUGUCCUAGCA	2484
rs2857790	7494	GCUAAGGAACAUC	733	7494	GCUAAGGAACAUC	733	7512	GAUGAUGAUGUCCUAGC	2485
rs2857790	7495	CUAAGGAACAUC	734	7495	CUAAGGAACAUC	734	7513	UGAUGAUGAUGUCCUAG	2486
rs2857790	7496	UAAGGAACAUC	735	7496	UAAGGAACAUC	735	7514	CUGAUGAUGAUGUCCUUA	2487
rs2857790	7497	AAGGAACAUC	736	7497	AAGGAACAUC	736	7515	GCUGAUGAUGAUGUCCUU	2488
rs362321	7665	GUUCAUCUACCGCAUCAAC	737	7665	GUUCAUCUACCGCAUCAAC	737	7683	GUUGAUGCGGUGAUGAAC	2489

rs362321	7666	UUCAUCUACCGCAUCAACA	738	7666	UUCAUCUACCGCAUCAACA	738	7684	UGUUGAUGCGGUAGAUGAA	2490
rs362321	7667	UCAUCUACCGCAUCAACAC	739	7667	UCAUCUACCGCAUCAACAC	739	7685	GUGUUGAUGCGGUAGAUGA	2491
rs362321	7668	CAUCUACCGCAUCAACACA	740	7668	CAUCUACCGCAUCAACACA	740	7686	UGUGUUGAUGCGGUAGAUG	2492
rs362321	7669	AUCUACCGCAUCAACACAC	741	7669	AUCUACCGCAUCAACACAC	741	7687	GUGUGUUGAUGCGGUAGAUG	2493
rs362321	7670	UCUACCGCAUCAACACACU	742	7670	UCUACCGCAUCAACACACU	742	7688	AGUGUGUUGAUGCGGUAGA	2494
rs362321	7671	CUACCGCAUCAACACACUA	743	7671	CUACCGCAUCAACACACUA	743	7689	UAGUGUGUUGAUGCGGUAG	2495
rs362321	7672	UACCGCAUCAACACACUAG	744	7672	UACCGCAUCAACACACUAG	744	7690	CUAGUGUGUUGAUGCGGUAG	2496
rs362321	7673	ACCGCAUCAACACACUAGG	745	7673	ACCGCAUCAACACACUAGG	745	7691	CCUAGUGUGUUGAUGCGGU	2497
rs362321	7674	CCGCAUCAACACACUAGGC	746	7674	CCGCAUCAACACACUAGGC	746	7692	GCCUAGUGUGUUGAUGCGG	2498
rs362321	7675	CGCAUCAACACACUAGGCU	747	7675	CGCAUCAACACACUAGGCU	747	7693	AGCCUAGUGUGUUGAUGCG	2499
rs362321	7676	GCAUCAACACACUAGGCUG	748	7676	GCAUCAACACACUAGGCUG	748	7694	CAGCCUAGUGUGUUGAUGC	2500
rs362321	7677	CAUCAACACACUAGGCUGG	749	7677	CAUCAACACACUAGGCUGG	749	7695	CCAGCCUAGUGUGUUGAUG	2501
rs362321	7678	AUCAACACACUAGGCUGGA	750	7678	AUCAACACACUAGGCUGGA	750	7696	UCCAGCCUAGUGUGUUGAU	2502
rs362321	7679	UCAACACACUAGGCUGGAC	751	7679	UCAACACACUAGGCUGGAC	751	7697	GUCCAGCCUAGUGUGUUGA	2503
rs362321	7680	CAACACACUAGGCUGGACC	752	7680	CAACACACUAGGCUGGACC	752	7698	GGUCCAGCCUAGUGUGUUG	2504
rs362321	7681	AACACACUAGGCUGGACCA	753	7681	AACACACUAGGCUGGACCA	753	7699	UGGUCCAGCCUAGUGUGUU	2505
rs362321	7682	ACACACUAGGCUGGACCAG	754	7682	ACACACUAGGCUGGACCAG	754	7700	CUGGUCCAGCCUAGUGUGU	2506
rs362321	7683	CACACUAGGCUGGACCAGU	755	7683	CACACUAGGCUGGACCAGU	755	7701	ACUGGUCCAGCCUAGUGUG	2507
rs362321	7665	GUUCAUCUACCGCAUCAAU	756	7665	GUUCAUCUACCGCAUCAAU	756	7683	AUUGAUGCGGUAGAUGAAC	2508
rs362321	7666	UUCAUCUACCGCAUCAUA	757	7666	UUCAUCUACCGCAUCAUA	757	7684	UAUUGAUGCGGUAGAUGAA	2509
rs362321	7667	UCAUCUACCGCAUCAAUAC	758	7667	UCAUCUACCGCAUCAAUAC	758	7685	GUAUUGAUGCGGUAGAUGA	2510
rs362321	7668	CAUCUACCGCAUCAAAUACA	759	7668	CAUCUACCGCAUCAAAUACA	759	7686	UGUAUUGAUGCGGUAGAUG	2511
rs362321	7669	AUCUACCGCAUCAAAUACAC	760	7669	AUCUACCGCAUCAAAUACAC	760	7687	GUGUAUUGAUGCGGUAGAUG	2512
rs362321	7670	UCUACCGCAUCAAAUACACU	761	7670	UCUACCGCAUCAAAUACACU	761	7688	AGUGUAUUGAUGCGGUAGA	2513
rs362321	7671	CUACCGCAUCAAAUACACUA	762	7671	CUACCGCAUCAAAUACACUA	762	7689	UAGUGUAUUGAUGCGGUAG	2514
rs362321	7672	UACCGCAUCAAAUACACUAG	763	7672	UACCGCAUCAAAUACACUAG	763	7690	CUAGUGUAUUGAUGCGGUAG	2515
rs362321	7673	ACCGCAUCAAAUACACUAGG	764	7673	ACCGCAUCAAAUACACUAGG	764	7691	CCUAGUGUAUUGAUGCGGU	2516
rs362321	7674	CCGCAUCAAAUACACUAGGC	765	7674	CCGCAUCAAAUACACUAGGC	765	7692	GCCUAGUGUAUUGAUGCGG	2517
rs362321	7675	CGCAUCAAAUACACUAGGCU	766	7675	CGCAUCAAAUACACUAGGCU	766	7693	AGCCUAGUGUAUUGAUGCG	2518
rs362321	7676	GCAUCAAAUACACUAGGCUG	767	7676	GCAUCAAAUACACUAGGCUG	767	7694	CAGCCUAGUGUAUUGAUGC	2519
rs362321	7677	CAUCAAAUACACUAGGCUGG	768	7677	CAUCAAAUACACUAGGCUGG	768	7695	CCAGCCUAGUGUAUUGAUG	2520
rs362321	7678	AUCAAAUACACUAGGCUGGA	769	7678	AUCAAAUACACUAGGCUGGA	769	7696	UCCAGCCUAGUGUAUUGAU	2521
rs362321	7679	UCAAAUACACUAGGCUGGAC	770	7679	UCAAAUACACUAGGCUGGAC	770	7697	GUCCAGCCUAGUGUAUUGA	2522
rs362321	7680	CAAAUACACUAGGCUGGACC	771	7680	CAAAUACACUAGGCUGGACC	771	7698	GGUCCAGCCUAGUGUAUUG	2523
rs362321	7681	AAUACACUAGGCUGGACCA	772	7681	AAUACACUAGGCUGGACCA	772	7699	UGGUCCAGCCUAGUGUAUU	2524
rs362321	7682	AUACACUAGGCUGGACCAG	773	7682	AUACACUAGGCUGGACCAG	773	7700	CUGGUCCAGCCUAGUGUAU	2525
rs362321	7683	UACACUAGGCUGGACCAGU	774	7683	UACACUAGGCUGGACCAGU	774	7701	ACUGGUCCAGCCUAGUGUA	2526
rs3025816	7735	CUUGGUGUCCUGGACGCG	775	7735	CUUGGUGUCCUGGACGCG	775	7753	GCGUACCCAGGACACCAAG	2527
rs3025816	7736	UUGGUGUCCUGGUGACGCA	776	7736	UUGGUGUCCUGGUGACGCA	776	7754	UGCGUACCCAGGACACCAA	2528

rs3025816	7737	UGGUGUCCUGGUGACGCAG	777	7737	UGGUGUCCUGGUGACGCAG	777	7755	CUGCGUACCCAGGACACCA	2529
rs3025816	7738	GGUGUCCUGGUGACGCAGC	778	7738	GGUGUCCUGGUGACGCAGC	778	7756	GCUGCGUACCCAGGACACC	2530
rs3025816	7739	GUGUCCUGGUGACGCAGCC	779	7739	GUGUCCUGGUGACGCAGCC	779	7757	GGCUGCGUACCCAGGACAC	2531
rs3025816	7740	UGUCCUGGUGACGCAGCCC	780	7740	UGUCCUGGUGACGCAGCCC	780	7758	GGCUGCGUACCCAGGACA	2532
rs3025816	7741	GUCCUGGUGACGCAGCCCC	781	7741	GUCCUGGUGACGCAGCCCC	781	7759	GGGGCUGCGUACCCAGGAC	2533
rs3025816	7742	UCCUGGUGACGCAGCCCCU	782	7742	UCCUGGUGACGCAGCCCCU	782	7760	AGGGCUGCGUACCCAGGA	2534
rs3025816	7743	CCUGGUGACGCAGCCCCUC	783	7743	CCUGGUGACGCAGCCCCUC	783	7761	GAGGGCUGCGUACCCAGG	2535
rs3025816	7744	CUGGUGACGCAGCCCCUCG	784	7744	CUGGUGACGCAGCCCCUCG	784	7762	CGAGGGCUGCGUACCCAG	2536
rs3025816	7745	UGGUGACGCAGCCCCUCGU	785	7745	UGGUGACGCAGCCCCUCGU	785	7763	ACGAGGGCUGCGUACCCA	2537
rs3025816	7746	GGUGACGCAGCCCCUCGUG	786	7746	GGUGACGCAGCCCCUCGUG	786	7764	CACGAGGGCUGCGUACCC	2538
rs3025816	7747	GUGACGCAGCCCCUCGUGA	787	7747	GUGACGCAGCCCCUCGUGA	787	7765	UCACGAGGGCUGCGUCAC	2539
rs3025816	7748	UGACGCAGCCCCUCGUGAU	788	7748	UGACGCAGCCCCUCGUGAU	788	7766	AUCACGAGGGCUGCGUCA	2540
rs3025816	7749	GACGCAGCCCCUCGUGAUG	789	7749	GACGCAGCCCCUCGUGAUG	789	7767	CAUCACGAGGGCUGCGUC	2541
rs3025816	7750	ACGCAGCCCCUCGUGAUGG	790	7750	ACGCAGCCCCUCGUGAUGG	790	7768	CCAUCACGAGGGCUGCGU	2542
rs3025816	7751	CGCAGCCCCUCGUGAUGGA	791	7751	CGCAGCCCCUCGUGAUGGA	791	7769	UCCAUCACGAGGGCUGCG	2543
rs3025816	7752	GCAGCCCCUCGUGAUGGAG	792	7752	GCAGCCCCUCGUGAUGGAG	792	7770	CUCCAUCACGAGGGCUGC	2544
rs3025816	7753	CAGCCCCUCGUGAUGGAGC	793	7753	CAGCCCCUCGUGAUGGAGC	793	7771	GCUCCAUCACGAGGGCUG	2545
rs3025816	7735	CUUGGUGUCCUGGUGACGU	794	7735	CUUGGUGUCCUGGUGACGU	794	7753	ACGUCACCCAGGACACCAAG	2546
rs3025816	7736	UUGGUGUCCUGGUGACGUA	795	7736	UUGGUGUCCUGGUGACGUA	795	7754	UACGUCACCCAGGACACCAA	2547
rs3025816	7737	UGGUGUCCUGGUGACGUAG	796	7737	UGGUGUCCUGGUGACGUAG	796	7755	CUACGUCACCCAGGACACCA	2548
rs3025816	7738	GGUGUCCUGGUGACGUAGC	797	7738	GGUGUCCUGGUGACGUAGC	797	7756	GUACGUCACCCAGGACACC	2549
rs3025816	7739	GUGUCCUGGUGACGUAGCC	798	7739	GUGUCCUGGUGACGUAGCC	798	7757	GGCUACGUCACCCAGGACAC	2550
rs3025816	7740	UGUCCUGGUGACGUAGCCC	799	7740	UGUCCUGGUGACGUAGCCC	799	7758	GGGCUACGUCACCCAGGACA	2551
rs3025816	7741	GUCCUGGUGACGUAGCCCC	800	7741	GUCCUGGUGACGUAGCCCC	800	7759	GGGGCUACGUCACCCAGGAC	2552
rs3025816	7742	UCCUGGUGACGUAGCCCCU	801	7742	UCCUGGUGACGUAGCCCCU	801	7760	AGGGGCUACGUCACCCAGGA	2553
rs3025816	7743	CCUGGUGACGUAGCCCCUC	802	7743	CCUGGUGACGUAGCCCCUC	802	7761	GAGGGGCUACGUCACCCAGG	2554
rs3025816	7744	CUGGUGACGUAGCCCCUCG	803	7744	CUGGUGACGUAGCCCCUCG	803	7762	CGAGGGGCUACGUCACCCAG	2555
rs3025816	7745	UGGUGACGUAGCCCCUCUGU	804	7745	UGGUGACGUAGCCCCUCUGU	804	7763	ACGAGGGGCUACGUCACCA	2556
rs3025816	7746	GGUGACGUAGCCCCUCUGUG	805	7746	GGUGACGUAGCCCCUCUGUG	805	7764	CACGAGGGGCUACGUCACC	2557
rs3025816	7747	GUGACGUAGCCCCUCUGUGA	806	7747	GUGACGUAGCCCCUCUGUGA	806	7765	UCACGAGGGGCUACGUCAC	2558
rs3025816	7748	UGACGUAGCCCCUCUGUGAU	807	7748	UGACGUAGCCCCUCUGUGAU	807	7766	AUCACGAGGGGCUACGUGA	2559
rs3025816	7749	GACGUAGCCCCUCUGUGAUG	808	7749	GACGUAGCCCCUCUGUGAUG	808	7767	CAUCACGAGGGGCUACGUC	2560
rs3025816	7750	ACGUAGCCCCUCUGUGAUGG	809	7750	ACGUAGCCCCUCUGUGAUGG	809	7768	CCAUCACGAGGGGCUACGU	2561
rs3025816	7751	CGUAGCCCCUCUGUGAUGGA	810	7751	CGUAGCCCCUCUGUGAUGGA	810	7769	UCCAUCACGAGGGGCUACG	2562
rs3025816	7752	GUAGCCCCUCUGUGAUGGAG	811	7752	GUAGCCCCUCUGUGAUGGAG	811	7770	CUCCAUCACGAGGGGCUAC	2563
rs3025816	7753	UAGCCCCUCUGUGAUGGAGC	812	7753	UAGCCCCUCUGUGAUGGAGC	812	7771	GCUCCAUCACGAGGGGCUA	2564
rs3025814	7831	CAGGCCAUCACCCUCACUGG	813	7831	CAGGCCAUCACCCUCACUGG	813	7849	CCAGUGAGGUGAUGGCCUG	2565
rs3025814	7832	AGGCCAUCACCCUCACUGGU	814	7832	AGGCCAUCACCCUCACUGGU	814	7850	ACCAGUGAGGUGAUGGCCU	2566
rs3025814	7833	GGCCAUCACCCUCACUGGUG	815	7833	GGCCAUCACCCUCACUGGUG	815	7851	CACCAGUGAGGUGAUGGCC	2567

rs3025814	7834	GCCAUCACCUACUGGUGC	816	7834	GCCAUCACCUACUGGUGC	816	7852	GCACCAGUGAGGUGAUGGC	2568
rs3025814	7835	CCAUCACCUACUGGUGCU	817	7835	CCAUCACCUACUGGUGCU	817	7853	AGCACCAGUGAGGUGAUGG	2569
rs3025814	7836	CAUCACCUACUGGUGCUC	818	7836	CAUCACCUACUGGUGCUC	818	7854	GAGCACCAGUGAGGUGAUG	2570
rs3025814	7837	AUCACCUACUGGUGCUCA	819	7837	AUCACCUACUGGUGCUCA	819	7855	UGAGCACCAGUGAGGUGAU	2571
rs3025814	7838	UCACCUACUGGUGCUCAG	820	7838	UCACCUACUGGUGCUCAG	820	7856	CUGAGCACCAGUGAGGUGA	2572
rs3025814	7839	CACCUCACUGGUGCUCAGU	821	7839	CACCUCACUGGUGCUCAGU	821	7857	ACUGAGCACCAGUGAGGUG	2573
rs3025814	7840	ACCUCACUGGUGCUCAGUG	822	7840	ACCUCACUGGUGCUCAGUG	822	7858	CACUGAGCACCAGUGAGGU	2574
rs3025814	7841	CCUCACUGGUGCUCAGUGC	823	7841	CCUCACUGGUGCUCAGUGC	823	7859	GCACUGAGCACCAGUGAGG	2575
rs3025814	7842	CUCACUGGUGCUCAGUGCA	824	7842	CUCACUGGUGCUCAGUGCA	824	7860	UGCACUGAGCACCAGUGAG	2576
rs3025814	7843	UCACUGGUGCUCAGUGCAA	825	7843	UCACUGGUGCUCAGUGCAA	825	7861	UUGCACUGAGCACCAGUGA	2577
rs3025814	7844	CACUGGUGCUCAGUGCAAU	826	7844	CACUGGUGCUCAGUGCAAU	826	7862	AUUGCACUGAGCACCAGUG	2578
rs3025814	7845	ACUGGUGCUCAGUGCAAUG	827	7845	ACUGGUGCUCAGUGCAAUG	827	7863	CAUUGCACUGAGCACCAGU	2579
rs3025814	7846	CUGGUGCUCAGUGCAAUGA	828	7846	CUGGUGCUCAGUGCAAUGA	828	7864	UCAUUGCACUGAGCACCAG	2580
rs3025814	7847	UGGUGCUCAGUGCAAUGAC	829	7847	UGGUGCUCAGUGCAAUGAC	829	7865	GUCAUUGCACUGAGCACC	2581
rs3025814	7848	GGUGCUCAGUGCAAUGACU	830	7848	GGUGCUCAGUGCAAUGACU	830	7866	AGUCAUUGCACUGAGCACC	2582
rs3025814	7849	GUGCUCAGUGCAAUGACUG	831	7849	GUGCUCAGUGCAAUGACUG	831	7867	CAGUCAUUGCACUGAGCAC	2583
rs3025814	7831	CAGGCCAUCACCUACUGC	832	7831	CAGGCCAUCACCUACUGC	832	7849	GCAGUGAGGUGAUGGCCUG	2584
rs3025814	7832	AGGCCAUCACCUACUGCU	833	7832	AGGCCAUCACCUACUGCU	833	7850	AGCAGUGAGGUGAUGGCCU	2585
rs3025814	7833	GGCCAUCACCUACUGCUG	834	7833	GGCCAUCACCUACUGCUG	834	7851	CAGCAGUGAGGUGAUGGCC	2586
rs3025814	7834	GCCAUCACCUACUGCUGC	835	7834	GCCAUCACCUACUGCUGC	835	7852	GCAGCAGUGAGGUGAUGGC	2587
rs3025814	7835	CCAUCACCUACUGCUGCU	836	7835	CCAUCACCUACUGCUGCU	836	7853	AGCAGCAGUGAGGUGAUGG	2588
rs3025814	7836	CAUCACCUACUGCUGCUC	837	7836	CAUCACCUACUGCUGCUC	837	7854	GAGCAGCAGUGAGGUGAUG	2589
rs3025814	7837	AUCACCUACUGCUGCUCA	838	7837	AUCACCUACUGCUGCUCA	838	7855	UGAGCAGCAGUGAGGUGAU	2590
rs3025814	7838	UCACCUACUGCUGCUCAG	839	7838	UCACCUACUGCUGCUCAG	839	7856	CUGAGCAGCAGUGAGGUGA	2591
rs3025814	7839	CACCUCACUGCUGCUCAGU	840	7839	CACCUCACUGCUGCUCAGU	840	7857	ACUGAGCAGCAGUGAGGUG	2592
rs3025814	7840	ACCUCACUGCUGCUCAGUG	841	7840	ACCUCACUGCUGCUCAGUG	841	7858	CACUGAGCAGCAGUGAGGU	2593
rs3025814	7841	CCUCACUGCUGCUCAGUGCA	842	7841	CCUCACUGCUGCUCAGUGCA	842	7859	GCACUGAGCAGCAGUGAGG	2594
rs3025814	7842	CUCACUGCUGCUCAGUGCAA	843	7842	CUCACUGCUGCUCAGUGCAA	843	7860	UGCACUGAGCAGCAGUGAG	2595
rs3025814	7843	UCACUGCUGCUCAGUGCAAU	844	7843	UCACUGCUGCUCAGUGCAAU	844	7861	UUGCACUGAGCAGCAGUGA	2596
rs3025814	7844	CACUGCUGCUCAGUGCAAUG	845	7844	CACUGCUGCUCAGUGCAAUG	845	7862	AUUGCACUGAGCAGCAGUG	2597
rs3025814	7845	ACUGCUGCUCAGUGCAAUGA	846	7845	ACUGCUGCUCAGUGCAAUGA	846	7863	CAUUGCACUGAGCAGCAGU	2598
rs3025814	7846	CUGCUGCUCAGUGCAAUGAC	847	7846	CUGCUGCUCAGUGCAAUGAC	847	7864	UCAUUGCACUGAGCAGCAG	2599
rs3025814	7847	UGCUGCUCAGUGCAAUGACU	848	7847	UGCUGCUCAGUGCAAUGACU	848	7865	GUCAUUGCACUGAGCAGCA	2600
rs3025814	7848	GCUGCUCAGUGCAAUGACU	849	7848	GCUGCUCAGUGCAAUGACU	849	7866	AGUCAUUGCACUGAGCAGC	2601
rs3025814	7849	CUGCUCAGUGCAAUGACUG	850	7849	CUGCUCAGUGCAAUGACUG	850	7867	CAGUCAUUGCACUGAGCAG	2602
rs362273	8100	CCACGAGAAAGCUGCUCUA	851	8100	CCACGAGAAAGCUGCUCUA	851	8118	UAGCAGCAGCUUCUCUGG	2603
rs362273	8101	CACGAGAAAGCUGCUCUAC	852	8101	CACGAGAAAGCUGCUCUAC	852	8119	GUAGCAGCAGCUUCUCUG	2604
rs362273	8102	ACGAGAAAGCUGCUCUACA	853	8102	ACGAGAAAGCUGCUCUACA	853	8120	UGUAGCAGCAGCUUCUCUG	2605
rs362273	8103	CGAGAAAGCUGCUCUACAG	854	8103	CGAGAAAGCUGCUCUACAG	854	8121	CUGUAGCAGCAGCUUCUCG	2606

rs362273	8104	GAGAAGCUGCUGCUACAGA	855	8104	GAGAAGCUGCUGCUACAGA	855	8122	UCUGUAGCAGCAGCUUCUC	2607
rs362273	8105	AGAAGCUGCUGCUACAGAU	856	8105	AGAAGCUGCUGCUACAGAU	856	8123	AUCUGUAGCAGCAGCUUCU	2608
rs362273	8106	GAAGCUGCUGCUACAGAU	857	8106	GAAGCUGCUGCUACAGAU	857	8124	GAUCUGUAGCAGCAGCUUC	2609
rs362273	8107	AAGCUGCUGCUACAGAU	858	8107	AAGCUGCUGCUACAGAU	858	8125	UGAUCUGUAGCAGCAGCUU	2610
rs362273	8108	AGCUGCUGCUACAGAUCAA	859	8108	AGCUGCUGCUACAGAUCAA	859	8126	UUGAUCUGUAGCAGCAGCU	2611
rs362273	8109	GCUGCUGCUACAGAUCAAC	860	8109	GCUGCUGCUACAGAUCAAC	860	8127	GUUGAUCUGUAGCAGCAGC	2612
rs362273	8110	CUGCUGCUACAGAUCAACC	861	8110	CUGCUGCUACAGAUCAACC	861	8128	GGUUGAUCUGUAGCAGCAG	2613
rs362273	8111	UGCUGCUACAGAUCAACCC	862	8111	UGCUGCUACAGAUCAACCC	862	8129	GGGUUGAUCUGUAGCAGCA	2614
rs362273	8112	GCUGCUACAGAUCAACCCC	863	8112	GCUGCUACAGAUCAACCCC	863	8130	GGGGUUGAUCUGUAGCAGC	2615
rs362273	8113	CUGCUACAGAUCAACCCCG	864	8113	CUGCUACAGAUCAACCCCG	864	8131	CGGGUUGAUCUGUAGCAG	2616
rs362273	8114	UGCUACAGAUCAACCCCGA	865	8114	UGCUACAGAUCAACCCCGA	865	8132	UCGGGUUGAUCUGUAGCA	2617
rs362273	8115	GUACAGAUCAACCCCGAG	866	8115	GUACAGAUCAACCCCGAG	866	8133	CUCGGGUUGAUCUGUAGC	2618
rs362273	8116	CUACAGAUCAACCCCGAGC	867	8116	CUACAGAUCAACCCCGAGC	867	8134	GCUCGGGUUGAUCUGUAG	2619
rs362273	8117	UACAGAUCAACCCCGAGCG	868	8117	UACAGAUCAACCCCGAGCG	868	8135	CGCUCGGGUUGAUCUGUA	2620
rs362273	8118	ACAGAUCAACCCCGAGCGG	869	8118	ACAGAUCAACCCCGAGCGG	869	8136	CCGUCGGGUUGAUCUGUG	2621
rs362273	8100	CCACGAGAGCUGUGCUG	870	8100	CCACGAGAGCUGUGCUG	870	8118	CAGCAGCAGCUUCUCGUG	2622
rs362273	8101	CACGAGAGCUGUGCUGC	871	8101	CACGAGAGCUGUGCUGC	871	8119	GCAGCAGCAGCUUCUCGUG	2623
rs362273	8102	ACGAGAGCUGUGCUGCA	872	8102	ACGAGAGCUGUGCUGCA	872	8120	UGCAGCAGCAGCUUCUCGU	2624
rs362273	8103	CGAGAGCUGUGCUGCAG	873	8103	CGAGAGCUGUGCUGCAG	873	8121	CUGCAGCAGCAGCUUCUCG	2625
rs362273	8104	GAGAAGCUGCUGCUGCAGA	874	8104	GAGAAGCUGCUGCUGCAGA	874	8122	UCUGCAGCAGCAGCUUCUC	2626
rs362273	8105	AGAAGCUGCUGCUGCAGAU	875	8105	AGAAGCUGCUGCUGCAGAU	875	8123	AUCUGCAGCAGCAGCUUCU	2627
rs362273	8106	GAAGCUGCUGCUGCAGAU	876	8106	GAAGCUGCUGCUGCAGAU	876	8124	GAUCUGCAGCAGCAGCUUC	2628
rs362273	8107	AAGCUGCUGCUGCAGAU	877	8107	AAGCUGCUGCUGCAGAU	877	8125	UGAUCUGCAGCAGCAGCUU	2629
rs362273	8108	AGCUGCUGCUGCAGAUCAA	878	8108	AGCUGCUGCUGCAGAUCAA	878	8126	UUGAUCUGCAGCAGCAGCU	2630
rs362273	8109	GCUGCUGCUGCAGAUCAAC	879	8109	GCUGCUGCUGCAGAUCAAC	879	8127	GUUGAUCUGCAGCAGCAGC	2631
rs362273	8110	CUGCUGCUGCAGAUCAACC	880	8110	CUGCUGCUGCAGAUCAACC	880	8128	GGUUGAUCUGCAGCAGCAG	2632
rs362273	8111	UGCUGCUGCAGAUCAACCC	881	8111	UGCUGCUGCAGAUCAACCC	881	8129	GGGUUGAUCUGCAGCAGCA	2633
rs362273	8112	GCUGCUGCAGAUCAACCCC	882	8112	GCUGCUGCAGAUCAACCCC	882	8130	GGGGUUGAUCUGCAGCAGC	2634
rs362273	8113	CUGCUGCAGAUCAACCCCG	883	8113	CUGCUGCAGAUCAACCCCG	883	8131	CGGGUUGAUCUGCAGCAG	2635
rs362273	8114	UGCUGCAGAUCAACCCCGA	884	8114	UGCUGCAGAUCAACCCCGA	884	8132	UCGGGUUGAUCUGCAGCA	2636
rs362273	8115	GCUGCAGAUCAACCCCGAG	885	8115	GCUGCAGAUCAACCCCGAG	885	8133	CUCGGGUUGAUCUGCAGC	2637
rs362273	8116	CUGCAGAUCAACCCCGAGC	886	8116	CUGCAGAUCAACCCCGAGC	886	8134	GCUCGGGUUGAUCUGCAG	2638
rs362273	8117	UGCAGAUCAACCCCGAGCG	887	8117	UGCAGAUCAACCCCGAGCG	887	8135	CCGUCGGGUUGAUCUGCA	2639
rs362273	8118	GCAGAUCAACCCCGAGCGG	888	8118	GCAGAUCAACCCCGAGCGG	888	8136	CCGUCGGGUUGAUCUGC	2640
HD-Ex58	8231	ACGAGGAAGAGGAGGAGGA	889	8231	ACGAGGAAGAGGAGGAGGA	889	8249	UCCUCCUCCUUCUCCUGU	2641
HD-Ex58	8232	CGAGGAAGAGGAGGAGGAG	890	8232	CGAGGAAGAGGAGGAGGAG	890	8250	CUCCUCCUCCUUCUCCUG	2642
HD-Ex58	8233	GAGGAAGAGGAGGAGGAGG	891	8233	GAGGAAGAGGAGGAGGAGG	891	8251	CCUCCUCCUCCUUCUCCU	2643
HD-Ex58	8234	AGGAAGAGGAGGAGGAGGC	892	8234	AGGAAGAGGAGGAGGAGGC	892	8252	GCCUCCUCCUCCUUCUCCU	2644
HD-Ex58	8235	GGAAGAGGAGGAGGAGGCC	893	8235	GGAAGAGGAGGAGGAGGCC	893	8253	GGCCUCCUCCUCCUCCUCC	2645

HD-Ex58	8236	GAAGAGGAGGAGGAGGCCG	894	8236	GAAGAGGAGGAGGAGGCCG	894	8254	CGGCCUCCUCCUCCUCCU	2646
HD-Ex58	8237	AAGAGGAGGAGGAGGCCGA	895	8237	AAGAGGAGGAGGAGGCCGA	895	8255	UCGGCCUCCUCCUCCUCCU	2647
HD-Ex58	8238	AGAGGAGGAGGAGGCCGAC	896	8238	AGAGGAGGAGGAGGCCGAC	896	8256	GUCGGCCUCCUCCUCCUCCU	2648
HD-Ex58	8239	GAGGAGGAGGAGGCCGACG	897	8239	GAGGAGGAGGAGGCCGACG	897	8257	CGUCGGCCUCCUCCUCCUCCU	2649
HD-Ex58	8240	AGGAGGAGGAGGCCGACGC	898	8240	AGGAGGAGGAGGCCGACGC	898	8258	GCGUCGGCCUCCUCCUCCUCCU	2650
HD-Ex58	8241	GGAGGAGGAGGCCGACGCC	899	8241	GGAGGAGGAGGCCGACGCC	899	8259	GGCGUCGGCCUCCUCCUCCUCC	2651
HD-Ex58	8231	ACGAGGAAGAGGAGGAGGC	900	8231	ACGAGGAAGAGGAGGAGGC	900	8249	GCCUCCUCCUCCUCCUCCUCCU	2652
HD-Ex58	8232	CGAGGAAGAGGAGGAGGCC	901	8232	CGAGGAAGAGGAGGAGGCC	901	8250	GGCCUCCUCCUCCUCCUCCUCC	2653
HD-Ex58	8233	GAGGAAGAGGAGGAGGCCG	902	8233	GAGGAAGAGGAGGAGGCCG	902	8251	CGGCCUCCUCCUCCUCCUCCU	2654
HD-Ex58	8234	AGGAAGAGGAGGAGGCCGA	903	8234	AGGAAGAGGAGGAGGCCGA	903	8252	UCGGCCUCCUCCUCCUCCUCCU	2655
HD-Ex58	8235	GGAAGAGGAGGAGGCCGAC	904	8235	GGAAGAGGAGGAGGCCGAC	904	8253	GUCGGCCUCCUCCUCCUCCUCC	2656
HD-Ex58	8236	GAAGAGGAGGAGGCCGACG	905	8236	GAAGAGGAGGAGGCCGACG	905	8254	CGUCGGCCUCCUCCUCCUCCU	2657
HD-Ex58	8237	AAGAGGAGGAGGCCGACGC	906	8237	AAGAGGAGGAGGCCGACGC	906	8255	GCGUCGGCCUCCUCCUCCUCCU	2658
HD-Ex58	8238	AGAGGAGGAGGCCGACGCC	907	8238	AGAGGAGGAGGCCGACGCC	907	8256	GGCGUCGGCCUCCUCCUCCUCC	2659
rs2276881	8460	GCGCAACCAGUUUGAGCUG	908	8460	GCGCAACCAGUUUGAGCUG	908	8478	CAGCUCACAAACUGGUUGCGC	2660
rs2276881	8461	CGCAACCAGUUUGAGCUGA	909	8461	CGCAACCAGUUUGAGCUGA	909	8479	UCAGCUCACAAACUGGUUGCG	2661
rs2276881	8462	GCAACCAGUUUGAGCUGAU	910	8462	GCAACCAGUUUGAGCUGAU	910	8480	AUCAGCUCACAAACUGGUUGC	2662
rs2276881	8463	CAACCAGUUUGAGCUGAUG	911	8463	CAACCAGUUUGAGCUGAUG	911	8481	CAUCAGCUCACAAACUGGUUG	2663
rs2276881	8464	AACCAGUUUGAGCUGAUGU	912	8464	AACCAGUUUGAGCUGAUGU	912	8482	ACAUCAGCUCACAAACUGGUU	2664
rs2276881	8465	ACCAGUUUGAGCUGAUGUA	913	8465	ACCAGUUUGAGCUGAUGUA	913	8483	UACAUCAGCUCACAAACUGGU	2665
rs2276881	8466	CCAGUUUGAGCUGAUGUUA	914	8466	CCAGUUUGAGCUGAUGUUA	914	8484	AUACAUCAGCUCACAAACUGG	2666
rs2276881	8467	CAGUUUGAGCUGAUGUAUG	915	8467	CAGUUUGAGCUGAUGUAUG	915	8485	CAUACAUCAGCUCACAAACUG	2667
rs2276881	8468	AGUUUGAGCUGAUGUAUGU	916	8468	AGUUUGAGCUGAUGUAUGU	916	8486	ACAUACAUCAGCUCACAAACU	2668
rs2276881	8469	GUUUGAGCUGAUGUAUGUG	917	8469	GUUUGAGCUGAUGUAUGUG	917	8487	CACAUAUAUCAGCUCACAAAC	2669
rs2276881	8470	UUUGAGCUGAUGUAUGUGA	918	8470	UUUGAGCUGAUGUAUGUGA	918	8488	UCACAUAUAUCAGCUCACAA	2670
rs2276881	8471	UUGAGCUGAUGUAUGUGAC	919	8471	UUGAGCUGAUGUAUGUGAC	919	8489	GUCACAUAUAUCAGCUCACAA	2671
rs2276881	8472	UGAGCUGAUGUAUGUGACG	920	8472	UGAGCUGAUGUAUGUGACG	920	8490	CGUCACAUAUAUCAGCUCAC	2672
rs2276881	8473	GAGCUGAUGUAUGUGACGC	921	8473	GAGCUGAUGUAUGUGACGC	921	8491	GGUCACAUAUAUCAGCUCUC	2673
rs2276881	8474	AGCUGAUGUAUGUGACGCU	922	8474	AGCUGAUGUAUGUGACGCU	922	8492	AGCGUCACAUAUAUCAGCUCU	2674
rs2276881	8475	GCUGAUGUAUGUGACGCGU	923	8475	GCUGAUGUAUGUGACGCGU	923	8493	CAGCGUCACAUAUAUCAGCAG	2675
rs2276881	8476	CUGAUGUAUGUGACGCGUGA	924	8476	CUGAUGUAUGUGACGCGUGA	924	8494	UCAGCGUCACAUAUAUCAGAG	2676
rs2276881	8477	UGAUGUAUGUGACGCGUGAC	925	8477	UGAUGUAUGUGACGCGUGAC	925	8495	GUCAGCGUCACAUAUAUCA	2677
rs2276881	8478	GAUGUAUGUGACGCGUGACA	926	8478	GAUGUAUGUGACGCGUGACA	926	8496	UGUCAGCGUCACAUAUAUCA	2678
rs2276881	8460	GCGCAACCAGUUUGAGCUGA	927	8460	GCGCAACCAGUUUGAGCUGA	927	8478	UAGCUCACAAACUGGUUGCGC	2679
rs2276881	8461	CGCAACCAGUUUGAGCUGAA	928	8461	CGCAACCAGUUUGAGCUGAA	928	8479	UUAGCUCACAAACUGGUUGCG	2680
rs2276881	8462	GCAACCAGUUUGAGCUGAAU	929	8462	GCAACCAGUUUGAGCUGAAU	929	8480	AUUAGCUCACAAACUGGUUGC	2681
rs2276881	8463	CAACCAGUUUGAGCUGAAUG	930	8463	CAACCAGUUUGAGCUGAAUG	930	8481	CAUUAGCUCACAAACUGGUUG	2682
rs2276881	8464	AACCAGUUUGAGCUGAAUGU	931	8464	AACCAGUUUGAGCUGAAUGU	931	8482	ACAUAGCUCACAAACUGGUU	2683
rs2276881	8465	ACCAGUUUGAGCUGAAUGUA	932	8465	ACCAGUUUGAGCUGAAUGUA	932	8483	UACAUAGCUCACAAACUGGU	2684

rs2276881	8466	CCAGUUUGAGCUAAUUGUAU	933	8466	CCAGUUUGAGCUAAUUGUAU	933	8484	AUACAUUAGCUCUAAACUGG	2685
rs2276881	8467	CAGUUUGAGCUAAUUGUAUG	934	8467	CAGUUUGAGCUAAUUGUAUG	934	8485	CAUACAUUAGCUCUAAACUG	2686
rs2276881	8468	AGUUUGAGCUAAUUGUAUGU	935	8468	AGUUUGAGCUAAUUGUAUGU	935	8486	ACAUACAUUAGCUCUAAACU	2687
rs2276881	8469	GUUUUGAGCUAAUUGUAUGUG	936	8469	GUUUUGAGCUAAUUGUAUGUG	936	8487	CACAUACAUUAGCUCUAAAC	2688
rs2276881	8470	UUUGAGCUAAUUGUAUGUGA	937	8470	UUUGAGCUAAUUGUAUGUGA	937	8488	UCACAUACAUUAGCUCUAAA	2689
rs2276881	8471	UUGAGCUAAUUGUAUGUGAC	938	8471	UUGAGCUAAUUGUAUGUGAC	938	8489	GUCACAUACAUUAGCUCUAA	2690
rs2276881	8472	UGAGCUAAUUGUAUGUGACG	939	8472	UGAGCUAAUUGUAUGUGACG	939	8490	CGUCACAUACAUUAGCUCU	2691
rs2276881	8473	GAGCUAAUUGUAUGUGACGC	940	8473	GAGCUAAUUGUAUGUGACGC	940	8491	GCGUCACAUACAUUAGCUC	2692
rs2276881	8474	AGCUAAUUGUAUGUGACGCU	941	8474	AGCUAAUUGUAUGUGACGCU	941	8492	AGCGUCACAUACAUUAGCU	2693
rs2276881	8475	GCUAUUGUAUGUGACGCUG	942	8475	GCUAUUGUAUGUGACGCUG	942	8493	CAGCGUCACAUACAUUAGC	2694
rs2276881	8476	CUAAUUGUAUGUGACGCUGA	943	8476	CUAAUUGUAUGUGACGCUGA	943	8494	UCAGCGUCACAUACAUUAG	2695
rs2276881	8477	UAAUUGUAUGUGACGCUGAC	944	8477	UAAUUGUAUGUGACGCUGAC	944	8495	GUCAGCGUCACAUACAUUA	2696
rs2276881	8478	AAUGUAUGUGACGCUGACA	945	8478	AAUGUAUGUGACGCUGACA	945	8496	UGUCAGCGUCACAUACAUU	2697
rs362272	8659	GUUGAGCCCCUGCACGGCG	946	8659	GUUGAGCCCCUGCACGGCG	946	8677	CGCCGUGCAGGGCUCUCAA	2698
rs362272	8660	UUGAGCCCCUGCACGGCGU	947	8660	UUGAGCCCCUGCACGGCGU	947	8678	ACGCCGUGCAGGGCUCUCAA	2699
rs362272	8661	UGGAGCCCCUGCACGGCGUC	948	8661	UGGAGCCCCUGCACGGCGUC	948	8679	GACGCCGUGCAGGGCUCUCC	2700
rs362272	8662	GGAGCCCCUGCACGGCGUCC	949	8662	GGAGCCCCUGCACGGCGUCC	949	8680	GGAGCCCCGUGCAGGGCUC	2701
rs362272	8663	GAGCCUGCACGGCGUCCU	950	8663	GAGCCUGCACGGCGUCCU	950	8681	AGGACCCGUGCAGGGCUC	2702
rs362272	8664	AGCCUGCACGGCGUCCUC	951	8664	AGCCUGCACGGCGUCCUC	951	8682	GAGGACCCGUGCAGGGCUC	2703
rs362272	8665	GCCUGCACGGCGUCCUCU	952	8665	GCCUGCACGGCGUCCUCU	952	8683	AGAGGACCCGUGCAGGGC	2704
rs362272	8666	CCUGCACGGCGUCCUCUA	953	8666	CCUGCACGGCGUCCUCUA	953	8684	UAGAGGACCCGUGCAGGG	2705
rs362272	8667	CCUGCACGGCGUCCUCUAU	954	8667	CCUGCACGGCGUCCUCUAU	954	8685	AUAGAGGACCCGUGCAGG	2706
rs362272	8668	CUGCACGGCGUCCUCUAUG	955	8668	CUGCACGGCGUCCUCUAUG	955	8686	CAUAGAGGACCCGUGCAG	2707
rs362272	8669	UGCACGGCGUCCUCUAUGU	956	8669	UGCACGGCGUCCUCUAUGU	956	8687	ACAUAGAGGACCCGUGCA	2708
rs362272	8670	GCACGGCGUCCUCUAUGUG	957	8670	GCACGGCGUCCUCUAUGUG	957	8688	CACAUAGAGGACCCGUGC	2709
rs362272	8671	CACGGCGUCCUCUAUGUC	958	8671	CACGGCGUCCUCUAUGUC	958	8689	GCACAUAGAGGACCCGUG	2710
rs362272	8672	ACGGCGUCCUCUAUGUCU	959	8672	ACGGCGUCCUCUAUGUCU	959	8690	AGCACAUAGAGGACCCGUG	2711
rs362272	8673	CGGGCGUCCUCUAUGUCUG	960	8673	CGGGCGUCCUCUAUGUCUG	960	8691	CAGCACAUAGAGGACCCG	2712
rs362272	8674	GGCGUCCUCUAUGUCUGG	961	8674	GGCGUCCUCUAUGUCUGG	961	8692	CCAGCACAUAGAGGACGCC	2713
rs362272	8675	GCGUCCUCUAUGUCUGGA	962	8675	GCGUCCUCUAUGUCUGGA	962	8693	UCCAGCACAUAGAGGACGC	2714
rs362272	8676	CGUCCUCUAUGUCUGGAG	963	8676	CGUCCUCUAUGUCUGGAG	963	8694	CUCCAGCACAUAGAGGACG	2715
rs362272	8677	GUCCUCUAUGUCUGGAGU	964	8677	GUCCUCUAUGUCUGGAGU	964	8695	ACUCCAGCACAUAGAGGAC	2716
rs362272	8659	GUUGAGCCCCUGCACGGCA	965	8659	GUUGAGCCCCUGCACGGCA	965	8677	UGCCGUGCAGGGCUCUCAA	2717
rs362272	8660	UUGAGCCCCUGCACGGCAU	966	8660	UUGAGCCCCUGCACGGCAU	966	8678	AUGCCGUGCAGGGCUCUCAA	2718
rs362272	8661	UGGAGCCCCUGCACGGCAUC	967	8661	UGGAGCCCCUGCACGGCAUC	967	8679	GAUGCCGUGCAGGGCUCU	2719
rs362272	8662	GGAGCCCCUGCACGGCAUCC	968	8662	GGAGCCCCUGCACGGCAUCC	968	8680	GGAUGCCGUGCAGGGCUC	2720
rs362272	8663	GAGCCUGCACGGCAUCCU	969	8663	GAGCCUGCACGGCAUCCU	969	8681	AGGAUGCCGUGCAGGGCUC	2721
rs362272	8664	AGCCUGCACGGCAUCCUC	970	8664	AGCCUGCACGGCAUCCUC	970	8682	GAGGAUGCCGUGCAGGGCUC	2722
rs362272	8665	GCCUGCACGGCAUCCUCU	971	8665	GCCUGCACGGCAUCCUCU	971	8683	AGAGGAUGCCGUGCAGGGC	2723

rs362272	8666	CCUGCACGGCAUCCUCUA	972	8666	CCUGCACGGCAUCCUCUA	972	8684	UAGAGGAUGCCGUGCAGGG	2724
rs362272	8667	CCUGCACGGCAUCCUCUAU	973	8667	CCUGCACGGCAUCCUCUAU	973	8685	AUAGAGGAUCCGUGCAGG	2725
rs362272	8668	CUGCACGGCAUCCUCUAUG	974	8668	CUGCACGGCAUCCUCUAUG	974	8686	CAUAGAGGAUCCGUGCAG	2726
rs362272	8669	UGCACGGCAUCCUCUAUGU	975	8669	UGCACGGCAUCCUCUAUGU	975	8687	ACAUAGAGGAUCCCGUGCA	2727
rs362272	8670	GCACGGCAUCCUCUAUGUG	976	8670	GCACGGCAUCCUCUAUGUG	976	8688	CACAUAGAGGAUCCCGUGC	2728
rs362272	8671	CACGGCAUCCUCUAUGUGC	977	8671	CACGGCAUCCUCUAUGUGC	977	8689	GCACAUAGAGGAUCCCGUG	2729
rs362272	8672	ACGGCAUCCUCUAUGUGCU	978	8672	ACGGCAUCCUCUAUGUGCU	978	8690	AGCACAUAGAGGAUCCCGU	2730
rs362272	8673	CGGCAUCCUCUAUGUGCUG	979	8673	CGGCAUCCUCUAUGUGCUG	979	8691	CAGCACAUAGAGGAUCCCG	2731
rs362272	8674	GGCAUCCUCUAUGUGCUGG	980	8674	GGCAUCCUCUAUGUGCUGG	980	8692	CCAGCACAUAGAGGAUCCG	2732
rs362272	8675	GCAUCCUCUAUGUGCUGGA	981	8675	GCAUCCUCUAUGUGCUGGA	981	8693	UCCAGCACAUAGAGGAUCC	2733
rs362272	8676	CAUCCUCUAUGUGCUGGAG	982	8676	CAUCCUCUAUGUGCUGGAG	982	8694	CUCCAGCACAUAGAGGAU	2734
rs362272	8677	AUCCUCUAUGUGCUGGAGU	983	8677	AUCCUCUAUGUGCUGGAGU	983	8695	ACUCCAGCACAUAGAGGAU	2735
rs3025807	9136	UCAGACCCUAAUCCUGCAG	984	9136	UCAGACCCUAAUCCUGCAG	984	9154	CUGCAGGAUAGGGGUCUGA	2736
rs3025807	9137	CAGACCCUAAUCCUGCAGC	985	9137	CAGACCCUAAUCCUGCAGC	985	9155	GCUGCAGGAUAGGGGUCUG	2737
rs3025807	9138	AGACCCUAAUCCUGCAGCC	986	9138	AGACCCUAAUCCUGCAGCC	986	9156	GGCUGCAGGAUAGGGGUCU	2738
rs3025807	9139	GACCCUAAUCCUGCAGCCC	987	9139	GACCCUAAUCCUGCAGCCC	987	9157	GGCUGCAGGAUAGGGGUC	2739
rs3025807	9140	ACCCUAAUCCUGCAGCCCC	988	9140	ACCCUAAUCCUGCAGCCCC	988	9158	GGGGCUGCAGGAUAGGGU	2740
rs3025807	9141	CCCUAAUCCUGCAGCCCCC	989	9141	CCCUAAUCCUGCAGCCCCC	989	9159	GGGGCUGCAGGAUAGGG	2741
rs3025807	9142	CCUAAUCCUGCAGCCCCCG	990	9142	CCUAAUCCUGCAGCCCCCG	990	9160	CGGGGCGCAGGAUAGG	2742
rs3025807	9143	CUAAUCCUGCAGCCCCCGA	991	9143	CUAAUCCUGCAGCCCCCGA	991	9161	UCGGGGCUGCAGGAUAG	2743
rs3025807	9144	UAUCCUGCAGCCCCCGGAC	992	9144	UAUCCUGCAGCCCCCGGAC	992	9162	GUCGGGGCUGCAGGAUUA	2744
rs3025807	9145	AUCCUGCAGCCCCCGGACA	993	9145	AUCCUGCAGCCCCCGGACA	993	9163	UGUCGGGGCUGCAGGAUU	2745
rs3025807	9146	AUCCUGCAGCCCCCGGACAG	994	9146	AUCCUGCAGCCCCCGGACAG	994	9164	CUGUCGGGGCUGCAGGAU	2746
rs3025807	9147	UCCUGCAGCCCCCGGACAGC	995	9147	UCCUGCAGCCCCCGGACAGC	995	9165	GCUGUCGGGGCUGCAGGA	2747
rs3025807	9148	CCUGCAGCCCCCGGACAGCG	996	9148	CCUGCAGCCCCCGGACAGCG	996	9166	CGCUGUCGGGGCUGCAGG	2748
rs3025807	9149	CUGCAGCCCCCGGACAGCGA	997	9149	CUGCAGCCCCCGGACAGCGA	997	9167	UCGCUGUCGGGGGCGUGCAG	2749
rs3025807	9150	UGCAGCCCCCGGACAGCGAG	998	9150	UGCAGCCCCCGGACAGCGAG	998	9168	CUCGCUGUCGGGGGCGUGCA	2750
rs3025807	9151	GCAGCCCCCGGACAGCGAGU	999	9151	GCAGCCCCCGGACAGCGAGU	999	9169	ACUCGCUGUCGGGGGCGUGC	2751
rs3025807	9152	CAGCCCCCGGACAGCGAGUC	1000	9152	CAGCCCCCGGACAGCGAGUC	1000	9170	UACUCGCUGUCGGGGGCGUG	2752
rs3025807	9153	AGCCCCCGGACAGCGAGUCA	1001	9153	AGCCCCCGGACAGCGAGUCA	1001	9171	UGACUCGCUGUCGGGGGCGU	2753
rs3025807	9154	GCCCCCGGACAGCGAGUCAG	1002	9154	GCCCCCGGACAGCGAGUCAG	1002	9172	CUGACUCGCUGUCGGGGGCG	2754
rs3025807	9136	UCAGACCCUAAUCCUGCAT	1003	9136	UCAGACCCUAAUCCUGCAT	1003	9154	AUGCAGGAUAGGGGUCUGA	2755
rs3025807	9137	CAGACCCUAAUCCUGCATC	1004	9137	CAGACCCUAAUCCUGCATC	1004	9155	GAUGCAGGAUAGGGGUCUG	2756
rs3025807	9138	AGACCCUAAUCCUGCATCC	1005	9138	AGACCCUAAUCCUGCATCC	1005	9156	GGAUGCAGGAUAGGGGUCU	2757
rs3025807	9139	GACCCUAAUCCUGCATCCC	1006	9139	GACCCUAAUCCUGCATCCC	1006	9157	GGGAUGCAGGAUAGGGGUC	2758
rs3025807	9140	ACCCUAAUCCUGCATCCCC	1007	9140	ACCCUAAUCCUGCATCCCC	1007	9158	GGGAUGCAGGAUAGGGU	2759
rs3025807	9141	CCCUAAUCCUGCATCCCCC	1008	9141	CCCUAAUCCUGCATCCCCC	1008	9159	GGGGGAUGCAGGAUAGGG	2760
rs3025807	9142	CCUAAUCCUGCATCCCCCG	1009	9142	CCUAAUCCUGCATCCCCCG	1009	9160	CGGGGAUGCAGGAUAGG	2761
rs3025807	9143	CUAAUCCUGCATCCCCCGGA	1010	9143	CUAAUCCUGCATCCCCCGGA	1010	9161	UCGGGGGAUGCAGGAUAG	2762

rs3025807	9144	UAAUCCUGCATCCCCGAC	1011	9144	UAAUCCUGCATCCCCGAC	1011	9162	GUCGGGGGAUGCAGGAUA	2763
rs3025807	9145	AUCCUGCATCCCCGACA	1012	9145	AUCCUGCATCCCCGACA	1012	9163	UGUCGGGGGAUGCAGGAU	2764
rs3025807	9146	AUCCUGCATCCCCGACAG	1013	9146	AUCCUGCATCCCCGACAG	1013	9164	CUGUCGGGGGAUGCAGGAU	2765
rs3025807	9147	UCCUGCATCCCCGACAGC	1014	9147	UCCUGCATCCCCGACAGC	1014	9165	GCUGUCGGGGGAUGCAGGA	2766
rs3025807	9148	CCUGCATCCCCCGACAGCG	1015	9148	CCUGCATCCCCCGACAGCG	1015	9166	CGCUGUCGGGGGAUGCAGG	2767
rs3025807	9149	CUGCATCCCCCGACAGCGA	1016	9149	CUGCATCCCCCGACAGCGA	1016	9167	UCGCUGUCGGGGGAUGCAG	2768
rs3025807	9150	UGCATCCCCCGACAGCGAG	1017	9150	UGCATCCCCCGACAGCGAG	1017	9168	CUCGCUGUCGGGGGAUGC	2769
rs3025807	9151	GCATCCCCCGACAGCGAGU	1018	9151	GCATCCCCCGACAGCGAGU	1018	9169	ACUCGCUGUCGGGGGAUGC	2770
rs3025807	9152	CATCCCCCGACAGCGAGUC	1019	9152	CATCCCCCGACAGCGAGUC	1019	9170	GACUCGCUGUCGGGGGAUC	2771
rs3025807	9153	ATCCCCCGACAGCGAGUCA	1020	9153	ATCCCCCGACAGCGAGUCA	1020	9171	UGACUCGCUGUCGGGGGAU	2772
rs3025807	9154	TCCCCCGACAGCGAGUCAG	1021	9154	TCCCCCGACAGCGAGUCAG	1021	9172	CUGACUCGCUGUCGGGGGA	2773
rs362308	9681	AGCCCCAGGAAGCCCAUAU	1022	9681	AGCCCCAGGAAGCCCAUAU	1022	9699	AUAUGGGCUUCCUGGGGCU	2774
rs362308	9682	GCCCCAGGAAGCCCAUAUC	1023	9682	GCCCCAGGAAGCCCAUAUC	1023	9700	GAUAUGGGCUUCCUGGGGC	2775
rs362308	9683	CCCCAGGAAGCCCAUAUCA	1024	9683	CCCCAGGAAGCCCAUAUCA	1024	9701	UGAUAUGGGCUUCCUGGGG	2776
rs362308	9684	CCAGGAAGCCCAUAUACAC	1025	9684	CCAGGAAGCCCAUAUACAC	1025	9702	GUGAUAUGGGCUUCCUGGG	2777
rs362308	9685	CCAGGAAGCCCAUAUACACC	1026	9685	CCAGGAAGCCCAUAUACACC	1026	9703	GGUGAUAUGGGCUUCCUGG	2778
rs362308	9686	CAGGAAGCCCAUAUACACCG	1027	9686	CAGGAAGCCCAUAUACACCG	1027	9704	CGGUGAUAUGGGCUUCCUG	2779
rs362308	9687	AGGAAGCCCAUAUACACCGG	1028	9687	AGGAAGCCCAUAUACACCGG	1028	9705	CCGGUGAUAUGGGCUUCCU	2780
rs362308	9688	GGAAGCCCAUAUACACCGGC	1029	9688	GGAAGCCCAUAUACACCGGC	1029	9706	GCCGGUGAUAUGGGCUUCC	2781
rs362308	9689	GAAGCCCAUAUACACCGGCU	1030	9689	GAAGCCCAUAUACACCGGCU	1030	9707	AGCCGGUGAUAUGGGCUUC	2782
rs362308	9690	AAGCCCAUAUACACCGGCUG	1031	9690	AAGCCCAUAUACACCGGCUG	1031	9708	CAGCCGGUGAUAUGGGCUU	2783
rs362308	9691	AGCCCAUAUACACCGGCUGC	1032	9691	AGCCCAUAUACACCGGCUGC	1032	9709	GCAGCCGGUGAUAUGGGCU	2784
rs362308	9692	GCCCAUAUACACCGGCUGCU	1033	9692	GCCCAUAUACACCGGCUGCU	1033	9710	AGCAGCCGGUGAUAUGGGC	2785
rs362308	9693	CCCAUAUACACCGGCUGCUG	1034	9693	CCCAUAUACACCGGCUGCUG	1034	9711	CAGCAGCCGGUGAUAUGGG	2786
rs362308	9694	CCAUAUACACCGGCUGCUGA	1035	9694	CCAUAUACACCGGCUGCUGA	1035	9712	UCAGCAGCCGGUGAUAUGG	2787
rs362308	9695	CAUAUACACCGGCUGCUGAC	1036	9695	CAUAUACACCGGCUGCUGAC	1036	9713	GUCAGCAGCCGGUGAUAUG	2788
rs362308	9696	AUAUACACCGGCUGCUGACU	1037	9696	AUAUACACCGGCUGCUGACU	1037	9714	AGUCAGCAGCCGGUGAUAU	2789
rs362308	9697	UAUACACCGGCUGCUGACUU	1038	9697	UAUACACCGGCUGCUGACUU	1038	9715	AAGUCAGCAGCCGGUGAUA	2790
rs362308	9698	AUACACCGGCUGCUGACUUG	1039	9698	AUACACCGGCUGCUGACUUG	1039	9716	CAAGUCAGCAGCCGGUGAU	2791
rs362308	9699	UCACCGGCUGCUGACUUGU	1040	9699	UCACCGGCUGCUGACUUGU	1040	9717	CAAAGUCAGCAGCCGGUGA	2792
rs362308	9681	AGCCCCAGGAAGCCCAUAC	1041	9681	AGCCCCAGGAAGCCCAUAC	1041	9699	GAUUGGGCUUCCUGGGGCU	2793
rs362308	9682	GCCCCAGGAAGCCCAUACC	1042	9682	GCCCCAGGAAGCCCAUACC	1042	9700	GGUAUGGGCUUCCUGGGGC	2794
rs362308	9683	CCCCAGGAAGCCCAUACCA	1043	9683	CCCCAGGAAGCCCAUACCA	1043	9701	UGGUAUGGGCUUCCUGGGG	2795
rs362308	9684	CCCAGGAAGCCCAUACCCAC	1044	9684	CCCAGGAAGCCCAUACCCAC	1044	9702	GUGGUAUGGGCUUCCUGGG	2796
rs362308	9685	CCAGGAAGCCCAUACCCACC	1045	9685	CCAGGAAGCCCAUACCCACC	1045	9703	GGUGUAUGGGCUUCCUGG	2797
rs362308	9686	CAGGAAGCCCAUACCCACCG	1046	9686	CAGGAAGCCCAUACCCACCG	1046	9704	CGGUGUAUGGGCUUCCUG	2798
rs362308	9687	AGGAAGCCCAUACCCACCGG	1047	9687	AGGAAGCCCAUACCCACCGG	1047	9705	CCGGUGUAUGGGCUUCCU	2799
rs362308	9688	GGAAGCCCAUACCCACCGGC	1048	9688	GGAAGCCCAUACCCACCGGC	1048	9706	GCCGGUGUAUGGGCUUCC	2800
rs362308	9689	GAAGCCCAUACCCACCGGCU	1049	9689	GAAGCCCAUACCCACCGGCU	1049	9707	AGCCGGUGUAUGGGGCUUC	2801

rs362308	9690	AAGCCCAUACCAACCGGCGUG	1050	9690	AAGCCCAUACCAACCGGCGUG	1050	9708	CAGCCGGUGGUAUAGGGCUU	2802
rs362308	9691	AGCCCAUACCAACCGGCGUGC	1051	9691	AGCCCAUACCAACCGGCGUGC	1051	9709	GCAGCCGGUGGUAUAGGGCU	2803
rs362308	9692	GCCCAUACCAACCGGCGUGCU	1052	9692	GCCCAUACCAACCGGCGUGCU	1052	9710	AGCAGCCGGUGGUAUAGGGC	2804
rs362308	9693	CCCAUACCAACCGGCGUGCUG	1053	9693	CCCAUACCAACCGGCGUGCUG	1053	9711	CAGCAGCCGGUGGUAUAGGG	2805
rs362308	9694	CCAUACCAACCGGCGUGCUGA	1054	9694	CCAUACCAACCGGCGUGCUGA	1054	9712	UCAGCAGCCGGUGGUAUAGG	2806
rs362308	9695	CAUACCAACCGGCGUGCUGAC	1055	9695	CAUACCAACCGGCGUGCUGAC	1055	9713	GUCAGCAGCCGGUGGUAUAG	2807
rs362308	9696	AUACCAACCGGCGUGCUGACU	1056	9696	AUACCAACCGGCGUGCUGACU	1056	9714	AGUCAGCAGCCGGUGGUAU	2808
rs362308	9697	UACCAACCGGCGUGCUGACUU	1057	9697	UACCAACCGGCGUGCUGACUU	1057	9715	AAGUCAGCAGCCGGUGGUA	2809
rs362308	9698	ACCACCGGCGUGCUGACUUG	1058	9698	ACCACCGGCGUGCUGACUUG	1058	9716	CAAGUCAGCAGCCGGUGGU	2810
rs362308	9699	CCACCGGCGUGCUGACUUGU	1059	9699	CCACCGGCGUGCUGACUUGU	1059	9717	ACAAGUCAGCAGCCGGUGG	2811
rs362307	9791	GGAGCCUUUGGAAGUCUGU	1060	9791	GGAGCCUUUGGAAGUCUGU	1060	9809	ACAGACUCCAAAGGCUCC	2812
rs362307	9792	GAGCCUUUGGAAGUCUGUG	1061	9792	GAGCCUUUGGAAGUCUGUG	1061	9810	CACAGACUCCAAAGGCUCC	2813
rs362307	9793	AGCCUUUGGAAGUCUGUGC	1062	9793	AGCCUUUGGAAGUCUGUGC	1062	9811	GCACAGACUCCAAAGGCU	2814
rs362307	9794	GCCUUUGGAAGUCUGUGCC	1063	9794	GCCUUUGGAAGUCUGUGCC	1063	9812	GGCACAGACUCCAAAGGC	2815
rs362307	9795	CCUUUGGAAGUCUGUGGCC	1064	9795	CCUUUGGAAGUCUGUGGCC	1064	9813	GGGCACAGACUCCAAAGG	2816
rs362307	9796	CUUUGGAAGUCUGUGGCCU	1065	9796	CUUUGGAAGUCUGUGGCCU	1065	9814	AGGGCACAGACUCCAAAG	2817
rs362307	9797	UUUGGAAGUCUGUGGCCUU	1066	9797	UUUGGAAGUCUGUGGCCUU	1066	9815	AAGGGCACAGACUCCAA	2818
rs362307	9798	UUGGAAGUCUGUGGCCUUUG	1067	9798	UUGGAAGUCUGUGGCCUUUG	1067	9816	CAAGGCACAGACUCCAA	2819
rs362307	9799	UGGAAGUCUGUGGCCUUUGU	1068	9799	UGGAAGUCUGUGGCCUUUGU	1068	9817	ACAAGGCACAGACUCCAA	2820
rs362307	9800	GGAAGUCUGUGGCCUUUGUG	1069	9800	GGAAGUCUGUGGCCUUUGUG	1069	9818	CACAAGGCACAGACUCC	2821
rs362307	9801	GAAGUCUGUGGCCUUUGUGC	1070	9801	GAAGUCUGUGGCCUUUGUGC	1070	9819	GCACAAGGCACAGACUCC	2822
rs362307	9802	AAGUCUGUGGCCUUUGUGCC	1071	9802	AAGUCUGUGGCCUUUGUGCC	1071	9820	GGCACAAAGGCACAGACU	2823
rs362307	9803	AGUCUGUGGCCUUUGUGGCC	1072	9803	AGUCUGUGGCCUUUGUGGCC	1072	9821	GGGCACAAAGGCACAGACU	2824
rs362307	9804	GUCUGUGGCCUUUGUGGCCU	1073	9804	GUCUGUGGCCUUUGUGGCCU	1073	9822	AGGGCACAAAGGCACAGAC	2825
rs362307	9805	UCUGUGGCCUUUGUGGCCUG	1074	9805	UCUGUGGCCUUUGUGGCCUG	1074	9823	CAGGGCACAAAGGCACAGA	2826
rs362307	9806	CUGUGGCCUUUGUGGCCUGC	1075	9806	CUGUGGCCUUUGUGGCCUGC	1075	9824	GCAGGGCACAAAGGCACAG	2827
rs362307	9807	UGUGGCCUUUGUGGCCUGCC	1076	9807	UGUGGCCUUUGUGGCCUGCC	1076	9825	GGCAGGGCACAAAGGCACA	2828
rs362307	9808	GUGGCCUUUGUGGCCUGCCU	1077	9808	GUGGCCUUUGUGGCCUGCCU	1077	9826	AGGCAGGGCACAAAGGGCAC	2829
rs362307	9809	UGCCCUUGUGGCCUGCCUC	1078	9809	UGCCCUUGUGGCCUGCCUC	1078	9827	GAGGCAGGGCACAAAGGGCA	2830
rs362307	9791	GGAGCCUUUGGAAGUCUGC	1079	9791	GGAGCCUUUGGAAGUCUGC	1079	9809	GCAGACUCCAAAGGCUCC	2831
rs362307	9792	GAGCCUUUGGAAGUCUGCG	1080	9792	GAGCCUUUGGAAGUCUGCG	1080	9810	CGCAGACUCCAAAGGCUCC	2832
rs362307	9793	AGCCUUUGGAAGUCUGCGC	1081	9793	AGCCUUUGGAAGUCUGCGC	1081	9811	GCGCAGACUCCAAAGGCU	2833
rs362307	9794	GCCUUUGGAAGUCUGCGCC	1082	9794	GCCUUUGGAAGUCUGCGCC	1082	9812	GGCGCAGACUCCAAAGGC	2834
rs362307	9795	CCUUUGGAAGUCUGCGCCC	1083	9795	CCUUUGGAAGUCUGCGCCC	1083	9813	GGCGCAGACUCCAAAGG	2835
rs362307	9796	CUUUGGAAGUCUGCGCCCCU	1084	9796	CUUUGGAAGUCUGCGCCCCU	1084	9814	AGGGCGCAGACUCCAAAG	2836
rs362307	9797	UUUGGAAGUCUGCGCCCCU	1085	9797	UUUGGAAGUCUGCGCCCCU	1085	9815	AAGGGCGCAGACUCCAA	2837
rs362307	9798	UUGGAAGUCUGCGCCCCUUG	1086	9798	UUGGAAGUCUGCGCCCCUUG	1086	9816	CAAGGGCGCAGACUCCAA	2838
rs362307	9799	UGGAAGUCUGCGCCCCUUGU	1087	9799	UGGAAGUCUGCGCCCCUUGU	1087	9817	ACAAGGGCGCAGACUCCAA	2839
rs362307	9800	GGAAGUCUGCGCCCCUUGUG	1088	9800	GGAAGUCUGCGCCCCUUGUG	1088	9818	CACAAGGGCGCAGACUCC	2840

rs362307	9801	GAAGUCUGCGCCCUUGGUC	1089	9801	GAAUCUCUGCGCCCUUGGUC	1089	9819	GCACAAGGCGCAGACUUC	2841
rs362307	9802	AAGUCUGCGCCCUUGGUC	1090	9802	AAGUCUGCGCCCUUGGUC	1090	9820	GGACAAGGCGCAGACUU	2842
rs362307	9803	AGUCUGCGCCCUUGGCCC	1091	9803	AGUCUGCGCCCUUGGCCC	1091	9821	GGGACAAGGCGCGACACU	2843
rs362307	9804	GUCUGCGCCCUUGGCCC	1092	9804	GUCUGCGCCCUUGGCCC	1092	9822	AGGGACAAGGCGCGAC	2844
rs362307	9805	UCUGCGCCCUUGGCCCUG	1093	9805	UCUGCGCCCUUGGCCCUG	1093	9823	CAGGGACAAGGCGCGACA	2845
rs362307	9806	CUGCGCCCUUGGCCCUGC	1094	9806	CUGCGCCCUUGGCCCUGC	1094	9824	GCAGGGCACAAAGGCGCAG	2846
rs362307	9807	UGCGCCCUUGGCCCUGCC	1095	9807	UGCGCCCUUGGCCCUGCC	1095	9825	GGCAGGGCACAAAGGCGCA	2847
rs362307	9808	CGCCCUUGGCCCUGCCU	1096	9808	CGCCCUUGGCCCUGCCU	1096	9826	AGGCAGGGCACAAAGGCGCG	2848
rs362307	9809	CGCCCUUGGCCCUGCCUC	1097	9809	CGCCCUUGGCCCUGCCUC	1097	9827	GAGGCAGGGCACAAAGGCGG	2849
rs362306	10046	GCUGGUUGUUGCCAGGUUG	1098	10046	GCUGGUUGUUGCCAGGUUG	1098	10064	CAACCCUGGCAACAACCAGC	2850
rs362306	10047	CUGGUUGUUGCCAGGUUGC	1099	10047	CUGGUUGUUGCCAGGUUGC	1099	10065	GCAACCCUGGCAACAACCAG	2851
rs362306	10048	UGGUUGUUGCCAGGUUGCA	1100	10048	UGGUUGUUGCCAGGUUGCA	1100	10066	UGCAACCCUGGCAACAACC	2852
rs362306	10049	GGUUGUUGCCAGGUUGCAG	1101	10049	GGUUGUUGCCAGGUUGCAG	1101	10067	CUGCAACCCUGGCAACAACC	2853
rs362306	10050	GUUGUUGCCAGGUUGCAGC	1102	10050	GUUGUUGCCAGGUUGCAGC	1102	10068	GCUGCAACCCUGGCAACAAC	2854
rs362306	10051	UUGUUGCCAGGUUGCAGCU	1103	10051	UUGUUGCCAGGUUGCAGCU	1103	10069	AGCUGCAACCCUGGCAACAA	2855
rs362306	10052	UGUUGCCAGGUUGCAGCUG	1104	10052	UGUUGCCAGGUUGCAGCUG	1104	10070	CAGCUGCAACCCUGGCAACA	2856
rs362306	10053	GUUGCCAGGUUGCAGCUGC	1105	10053	GUUGCCAGGUUGCAGCUGC	1105	10071	GCAGCUGCAACCCUGGCAAC	2857
rs362306	10054	UUGCCAGGUUGCAGCUGCU	1106	10054	UUGCCAGGUUGCAGCUGCU	1106	10072	AGCAGCUGCAACCCUGGCAA	2858
rs362306	10055	UGCCAGGUUGCAGCUGCUC	1107	10055	UGCCAGGUUGCAGCUGCUC	1107	10073	GAGCAGCUGCAACCCUGGCA	2859
rs362306	10056	GCCAGGUUGCAGCUGCUCU	1108	10056	GCCAGGUUGCAGCUGCUCU	1108	10074	AGAGCAGCUGCAACCCUGGC	2860
rs362306	10057	CCAGGUUGCAGCUGCUCUU	1109	10057	CCAGGUUGCAGCUGCUCUU	1109	10075	AAGAGCAGCUGCAACCCUGG	2861
rs362306	10058	CAGGUUGCAGCUGCUCUUG	1110	10058	CAGGUUGCAGCUGCUCUUG	1110	10076	CAAGAGCAGCUGCAACCCUG	2862
rs362306	10059	AGGUUGCAGCUGCUCUUGC	1111	10059	AGGUUGCAGCUGCUCUUGC	1111	10077	GCAAGAGCAGCUGCAACCU	2863
rs362306	10060	GGUUGCAGCUGCUCUUGCA	1112	10060	GGUUGCAGCUGCUCUUGCA	1112	10078	UGCAAGAGCAGCUGCAACC	2864
rs362306	10061	GUUGCAGCUGCUCUUGCAU	1113	10061	GUUGCAGCUGCUCUUGCAU	1113	10079	AUGCAAGAGCAGCUGCAAC	2865
rs362306	10062	UUGCAGCUGCUCUUGCAUC	1114	10062	UUGCAGCUGCUCUUGCAUC	1114	10080	GAUGCAAGAGCAGCUGCAA	2866
rs362306	10063	UGCAGCUGCUCUUGCAUCU	1115	10063	UGCAGCUGCUCUUGCAUCU	1115	10081	AGAUGCAAGAGCAGCUGCA	2867
rs362306	10064	GCAGCUGCUCUUGCAUCUG	1116	10064	GCAGCUGCUCUUGCAUCUG	1116	10082	CAGAUGCAAGAGCAGCUGC	2868
rs362306	10046	GCUGGUUGUUGCCAGGUUA	1117	10046	GCUGGUUGUUGCCAGGUUA	1117	10064	UAACCCUGGCAACAACCAGC	2869
rs362306	10047	CUGGUUGUUGCCAGGUUAC	1118	10047	CUGGUUGUUGCCAGGUUAC	1118	10065	GUAAACCCUGGCAACAACC	2870
rs362306	10048	UGGUUGUUGCCAGGUUACA	1119	10048	UGGUUGUUGCCAGGUUACA	1119	10066	UGUAACCCUGGCAACAACC	2871
rs362306	10049	GGUUGUUGCCAGGUUACAG	1120	10049	GGUUGUUGCCAGGUUACAG	1120	10067	CUGUAACCCUGGCAACAACC	2872
rs362306	10050	GUUGUUGCCAGGUUACAGC	1121	10050	GUUGUUGCCAGGUUACAGC	1121	10068	GCUGUAACCCUGGCAACAAC	2873
rs362306	10051	UUGUUGCCAGGUUACAGCU	1122	10051	UUGUUGCCAGGUUACAGCU	1122	10069	AGCUGUAACCCUGGCAACA	2874
rs362306	10052	UGUUGCCAGGUUACAGCUG	1123	10052	UGUUGCCAGGUUACAGCUG	1123	10070	CAGCUGUAACCCUGGCAACA	2875
rs362306	10053	GUUGCCAGGUUACAGCUGC	1124	10053	GUUGCCAGGUUACAGCUGC	1124	10071	GCAGCUGUAACCCUGGCAAC	2876
rs362306	10054	UUGCCAGGUUACAGCUGCU	1125	10054	UUGCCAGGUUACAGCUGCU	1125	10072	AGCAGCUGUAACCCUGGCAA	2877
rs362306	10055	UGCCAGGUUACAGCUGCUC	1126	10055	UGCCAGGUUACAGCUGCUC	1126	10073	GAGCAGCUGUAACCCUGGCA	2878
rs362306	10056	GCCAGGUUACAGCUGCUCU	1127	10056	GCCAGGUUACAGCUGCUCU	1127	10074	AGAGCAGCUGUAACCCUGGC	2879

rs362306	10057	CCAGGUUACAGCUGCUCUU	1128	10057	CCAGGUUACAGCUGCUCUU	1128	10075	AAGAGCAGCUGUAACCCUGG	2880
rs362306	10058	CAGGUUACAGCUGCUCUUG	1129	10058	CAGGUUACAGCUGCUCUUG	1129	10076	CAAGAGCAGCUGUAACCCUG	2881
rs362306	10059	AGGUUACAGCUGCUCUUGC	1130	10059	AGGUUACAGCUGCUCUUGC	1130	10077	GCAAGAGCAGCUGUAACCCU	2882
rs362306	10060	GGUUACAGCUGCUCUUGCA	1131	10060	GGUUACAGCUGCUCUUGCA	1131	10078	UGCAAGAGCAGCUGUAACC	2883
rs362306	10061	GUUACAGCUGCUCUUGCAU	1132	10061	GUUACAGCUGCUCUUGCAU	1132	10079	AUGCAAGAGCAGCUGUAAC	2884
rs362306	10062	UUACAGCUGCUCUUGCAUC	1133	10062	UUACAGCUGCUCUUGCAUC	1133	10080	GAUGCAAGAGCAGCUGUA	2885
rs362306	10063	UACAGCUGCUCUUGCAUCU	1134	10063	UACAGCUGCUCUUGCAUCU	1134	10081	AGAUGCAAGAGCAGCUGUA	2886
rs362306	10064	ACAGCUGCUCUUGCAUCUG	1135	10064	ACAGCUGCUCUUGCAUCUG	1135	10082	CAGAUGCAAGAGCAGCUGU	2887
rs362268	10094	CUCCUCCUGCAGGUGGC	1136	10094	CUCCUCCUGCAGGUGGC	1136	10112	GCCAGCCUGCAGGAGGGAG	2888
rs362268	10095	UCCUCCUGCAGGUGGC	1137	10095	UCCUCCUGCAGGUGGC	1137	10113	AGCCAGCCUGCAGGAGGGGA	2889
rs362268	10096	CCUCCUGCAGGUGGCUG	1138	10096	CCUCCUGCAGGUGGCUG	1138	10114	CAGCCAGCCUGCAGGAGGG	2890
rs362268	10097	CCUCCUGCAGGUGGCUGU	1139	10097	CCUCCUGCAGGUGGCUGU	1139	10115	ACAGCCAGCCUGCAGGAGG	2891
rs362268	10098	CUCCUGCAGGUGGCUGUU	1140	10098	CUCCUGCAGGUGGCUGUU	1140	10116	AACAGCCAGCCUGCAGGAG	2892
rs362268	10099	UCCUGCAGGUGGCUGUUG	1141	10099	UCCUGCAGGUGGCUGUUG	1141	10117	CAACAGCCAGCCUGCAGGA	2893
rs362268	10100	CCUGCAGGUGGCUGUUGG	1142	10100	CCUGCAGGUGGCUGUUGG	1142	10118	CCAACAGCCAGCCUGCAGG	2894
rs362268	10101	CUGCAGGUGGCUGUUGGC	1143	10101	CUGCAGGUGGCUGUUGGC	1143	10119	GCCAACAGCCAGCCUGCAG	2895
rs362268	10102	UGCAGGUGGCUGUUGGCC	1144	10102	UGCAGGUGGCUGUUGGCC	1144	10120	GGCCAACAGCCAGCCUGCA	2896
rs362268	10103	GCAGGUGGCUGUUGGCC	1145	10103	GCAGGUGGCUGUUGGCC	1145	10121	GGCCAACAGCCAGCCUGC	2897
rs362268	10104	CAGGUGGCUGUUGGCC	1146	10104	CAGGUGGCUGUUGGCC	1146	10122	GGGCCAACAGCCAGCCUG	2898
rs362268	10105	AGGUGGCUGUUGGCC	1147	10105	AGGUGGCUGUUGGCC	1147	10123	AGGGCCAACAGCCAGCCU	2899
rs362268	10106	GGCUGGCUGUUGGCC	1148	10106	GGCUGGCUGUUGGCC	1148	10124	GAGGGCCAACAGCCAGCC	2900
rs362268	10107	GCUGGCUGUUGGCC	1149	10107	GCUGGCUGUUGGCC	1149	10125	AGAGGGCCAACAGCCAGC	2901
rs362268	10108	CUGGCUGUUGGCC	1150	10108	CUGGCUGUUGGCC	1150	10126	CAGAGGGCCAACAGCCAG	2902
rs362268	10109	UGGCUGUUGGCC	1151	10109	UGGCUGUUGGCC	1151	10127	GCAGAGGGCCAACAGCCA	2903
rs362268	10110	GGCUGUUGGCC	1152	10110	GGCUGUUGGCC	1152	10128	AGCAGAGGGCCAACAGCC	2904
rs362268	10111	GCUGUUGGCC	1153	10111	GCUGUUGGCC	1153	10129	CAGCAGAGGGCCAACAGC	2905
rs362268	10112	CUGUUGGCC	1154	10112	CUGUUGGCC	1154	10130	ACAGCAGAGGGCCAACAG	2906
rs362268	10094	CUCCUCCUGCAGGUGGC	1155	10094	CUCCUCCUGCAGGUGGC	1155	10112	CCCAGCCUGCAGGAGGGAG	2907
rs362268	10095	UCCUCCUGCAGGUGGU	1156	10095	UCCUCCUGCAGGUGGU	1156	10113	ACCCAGCCUGCAGGAGGGGA	2908
rs362268	10096	CCUCCUGCAGGUGGGUG	1157	10096	CCUCCUGCAGGUGGGUG	1157	10114	CACCCAGCCUGCAGGAGGG	2909
rs362268	10097	CCUCCUGCAGGUGGGUGU	1158	10097	CCUCCUGCAGGUGGGUGU	1158	10115	ACACCCAGCCUGCAGGAGG	2910
rs362268	10098	CUCCUGCAGGUGGGUGUU	1159	10098	CUCCUGCAGGUGGGUGUU	1159	10116	AACACCCAGCCUGCAGGAG	2911
rs362268	10099	UCCUGCAGGUGGGUGUUG	1160	10099	UCCUGCAGGUGGGUGUUG	1160	10117	CAACACCCAGCCUGCAGGA	2912
rs362268	10100	CCUGCAGGUGGGUGUUGG	1161	10100	CCUGCAGGUGGGUGUUGG	1161	10118	CCAACACCCAGCCUGCAGG	2913
rs362268	10101	CUGCAGGUGGGUGUUGGC	1162	10101	CUGCAGGUGGGUGUUGGC	1162	10119	GCCAACACCCAGCCUGCAG	2914
rs362268	10102	UGCAGGUGGGUGUUGGCC	1163	10102	UGCAGGUGGGUGUUGGCC	1163	10120	GGCCAACACCCAGCCUGCA	2915
rs362268	10103	GCAGGUGGGUGUUGGCC	1164	10103	GCAGGUGGGUGUUGGCC	1164	10121	GGGCCAACACCCAGCCUGC	2916
rs362268	10104	CAGGUGGGUGUUGGCC	1165	10104	CAGGUGGGUGUUGGCC	1165	10122	GGGGCCAACACCCAGCCUG	2917
rs362268	10105	AGGUGGGUGUUGGCC	1166	10105	AGGUGGGUGUUGGCC	1166	10123	AGGGCCAACACCCAGCCU	2918

rs362305	10113	UGUUGGCCCCUCUGCUGUC	1167	10113	UGUUGGCCCCUCUGCUGUC	1167	10131	GACAGCAGAGGGGGCCAACA	2919
rs362305	10114	GUUGGCCCCUCUGCUGUC	1168	10114	GUUGGCCCCUCUGCUGUC	1168	10132	GGACAGCAGAGGGGGCCAAC	2920
rs362305	10115	UUGGCCCCUCUGCUGUCU	1169	10115	UUGGCCCCUCUGCUGUCU	1169	10133	AGGACAGCAGAGGGGGCCAA	2921
rs362305	10116	UGGCCCCUCUGCUGUCUG	1170	10116	UGGCCCCUCUGCUGUCUG	1170	10134	CAGGACAGCAGAGGGGGCCA	2922
rs362305	10117	GGCCCCUCUGCUGUCUGC	1171	10117	GGCCCCUCUGCUGUCUGC	1171	10135	GCAGGACAGCAGAGGGGGCC	2923
rs362305	10118	GCCCCUCUGCUGUCUGCA	1172	10118	GCCCCUCUGCUGUCUGCA	1172	10136	UGCAGGACAGCAGAGGGGGC	2924
rs362305	10119	CCCCUCUGCUGUCUGCAG	1173	10119	CCCCUCUGCUGUCUGCAG	1173	10137	CUGCAGGACAGCAGAGGGG	2925
rs362305	10120	CCUCUCUGCUGUCUGCAGU	1174	10120	CCUCUCUGCUGUCUGCAGU	1174	10138	ACUGCAGGACAGCAGAGGG	2926
rs362305	10121	CCUCUGCUGUCUGCAGUA	1175	10121	CCUCUGCUGUCUGCAGUA	1175	10139	UACUGCAGGACAGCAGAGG	2927
rs362305	10122	CUCUGCUGUCUGCAGUAG	1176	10122	CUCUGCUGUCUGCAGUAG	1176	10140	CUACUGCAGGACAGCAGAG	2928
rs362305	10123	UCUGCUGUCUGCAGUAGA	1177	10123	UCUGCUGUCUGCAGUAGA	1177	10141	UCUACUGCAGGACAGCAG	2929
rs362305	10124	CUGCUGUCUGCAGUAGAA	1178	10124	CUGCUGUCUGCAGUAGAA	1178	10142	UUUACUGCAGGACAGCAGC	2930
rs362305	10106	GGCUGGCUUGGGCCCCUG	1179	10106	GGCUGGCUUGGGCCCCUG	1179	10124	CAGGGGCCAACAGCCAGCC	2931
rs362305	10107	GCUGGCUUGGGCCCCUGU	1180	10107	GCUGGCUUGGGCCCCUGU	1180	10125	ACAGGGGCCAACAGCCAGC	2932
rs362305	10108	CUGGCUUGGGCCCCUGUG	1181	10108	CUGGCUUGGGCCCCUGUG	1181	10126	CACAGGGGCCAACAGCCAG	2933
rs362305	10109	UGGCUUGGGCCCCUGUGC	1182	10109	UGGCUUGGGCCCCUGUGC	1182	10127	GCACAGGGGCCAACAGCCA	2934
rs362305	10110	GGCUGUUGGGCCCCUGUCU	1183	10110	GGCUGUUGGGCCCCUGUCU	1183	10128	AGCACAGGGGCCAACAGCC	2935
rs362305	10111	GCUGUUGGGCCCCUGUCUG	1184	10111	GCUGUUGGGCCCCUGUCUG	1184	10129	CAGCACAGGGGCCAACAGC	2936
rs362305	10112	CUGUUGGGCCCCUGUCUGU	1185	10112	CUGUUGGGCCCCUGUCUGU	1185	10130	ACAGCACAGGGGCCAACAG	2937
rs362305	10113	UGUUGGCCCCUCUGCUGUC	1186	10113	UGUUGGCCCCUCUGCUGUC	1186	10131	GACAGCACAGGGGGCCAACA	2938
rs362305	10114	GUUGGCCCCUCUGCUGUC	1187	10114	GUUGGCCCCUCUGCUGUC	1187	10132	GGACAGCACAGGGGGCCAAC	2939
rs362305	10115	UUGGCCCCUCUGCUGUCU	1188	10115	UUGGCCCCUCUGCUGUCU	1188	10133	AGGACAGCACAGGGGGCCA	2940
rs362305	10116	UGGCCCCUCUGCUGUCUG	1189	10116	UGGCCCCUCUGCUGUCUG	1189	10134	CAGGACAGCACAGGGGGCCA	2941
rs362305	10117	GGCCCCUCUGCUGUCUGC	1190	10117	GGCCCCUCUGCUGUCUGC	1190	10135	GCAGGACAGCACAGGGGGC	2942
rs362305	10118	GCCCCUCUGCUGUCUGCA	1191	10118	GCCCCUCUGCUGUCUGCA	1191	10136	UGCAGGACAGCACAGGGG	2943
rs362305	10119	CCCCUCUGCUGUCUGCAG	1192	10119	CCCCUCUGCUGUCUGCAG	1192	10137	CUGCAGGACAGCACAGGGG	2944
rs362305	10120	CCUCUGCUGUCUGCAGU	1193	10120	CCUCUGCUGUCUGCAGU	1193	10138	ACUGCAGGACAGCACAGGG	2945
rs362305	10121	CCUGCUGUCUGCAGUAGA	1194	10121	CCUGCUGUCUGCAGUAGA	1194	10139	UACUGCAGGACAGCACAGG	2946
rs362305	10122	CUGGCUUGCUGCAGUAG	1195	10122	CUGGCUUGCUGCAGUAG	1195	10140	CUACUGCAGGACAGCACAG	2947
rs362305	10123	UGUGCUGUCUGCAGUAGA	1196	10123	UGUGCUGUCUGCAGUAGA	1196	10141	UCUACUGCAGGACAGCAC	2948
rs362305	10124	GUGCUGUCUGCAGUAGAA	1197	10124	GUGCUGUCUGCAGUAGAA	1197	10142	UUUACUGCAGGACAGCAC	2949
rs362304	10218	AUGCACAGAUGCCAUUGGCC	1198	10218	AUGCACAGAUGCCAUUGGCC	1198	10236	GGCCAUUGGCAUCUGCAU	2950
rs362304	10219	UGCACAGAUGCCAUUGGCCU	1199	10219	UGCACAGAUGCCAUUGGCCU	1199	10237	AGGCCAUUGGCAUCUGCA	2951
rs362304	10220	GCACAGAUGCCAUUGGCCUG	1200	10220	GCACAGAUGCCAUUGGCCUG	1200	10238	CAGGCCAUUGGCAUCUGUG	2952
rs362304	10221	CACAGAUGCCAUUGGCCUGU	1201	10221	CACAGAUGCCAUUGGCCUGU	1201	10239	ACAGGCCAUUGGCAUCUGUG	2953
rs362304	10222	ACAGAUGCCAUUGGCCUGUG	1202	10222	ACAGAUGCCAUUGGCCUGUG	1202	10240	CACAGGCCAUUGGCAUCUGU	2954
rs362304	10223	CAGAUGCCAUUGGCCUGUGC	1203	10223	CAGAUGCCAUUGGCCUGUGC	1203	10241	GCACAGGCCAUUGGCAUCUG	2955
rs362304	10224	AGAUGCCAUUGGCCUGUGCU	1204	10224	AGAUGCCAUUGGCCUGUGCU	1204	10242	AGCACAGGCCAUUGGCAUCU	2956
rs362304	10225	GAUGCCAUUGGCCUGUGCUG	1205	10225	GAUGCCAUUGGCCUGUGCUG	1205	10243	CAGCACAGGCCAUUGGCAUC	2957

rs362304	10226	AUGCCAUGGCCUGUGGCGG	1206	10226	AUGCCAUGGCCUGUGGCGG	1206	10244	CCAGCACAGGCCAUGGCAU	2958
rs362304	10227	UGCCAUGGCCUGUGGCGG	1207	10227	UGCCAUGGCCUGUGGCGG	1207	10245	CCAGCACAGGCCAUGGCA	2959
rs362304	10228	GCCAUGGCCUGUGGCGG	1208	10228	GCCAUGGCCUGUGGCGG	1208	10246	GCCAGCACAGGCCAUGGC	2960
rs362304	10229	CCAUGGCCUGUGGCGG	1209	10229	CCAUGGCCUGUGGCGG	1209	10247	GCCAGCACAGGCCAUGG	2961
rs362304	10230	CAUGGCCUGUGGCGGCA	1210	10230	CAUGGCCUGUGGCGGCA	1210	10248	UGGCCAGCACAGGCCAUG	2962
rs362304	10231	AUGGCCUGUGGCGGCG	1211	10231	AUGGCCUGUGGCGGCG	1211	10249	CUGGCCAGCACAGGCCAU	2963
rs362304	10232	UGGCCUGUGGCGGCGAG	1212	10232	UGGCCUGUGGCGGCGAG	1212	10250	ACUGGCCAGCACAGGCCA	2964
rs362304	10233	GGCCUGUGGCGGCGAGUG	1213	10233	GGCCUGUGGCGGCGAGUG	1213	10251	CACUGGCCAGCACAGGCC	2965
rs362304	10234	CCUGUGUGGCGGCGAGUGG	1214	10234	CCUGUGUGGCGGCGAGUGG	1214	10252	CCACUGGCCAGCACAGGC	2966
rs362304	10235	CCUGUGUGGCGGCGAGUGG	1215	10235	CCUGUGUGGCGGCGAGUGG	1215	10253	GCCACUGGCCAGCACAGG	2967
rs362304	10236	CUGUGUGGCGGCGAGUGGCU	1216	10236	CUGUGUGGCGGCGAGUGGCU	1216	10254	AGCCACUGGCCAGCACAG	2968
rs362304	10218	AUGCACAGAUGCCAUGGCA	1217	10218	AUGCACAGAUGCCAUGGCA	1217	10236	UGCCAUGGCAUCUGUGCAU	2969
rs362304	10219	UGCACAGAUGCCAUGGCAU	1218	10219	UGCACAGAUGCCAUGGCAU	1218	10237	AUGCCAUGGCAUCUGUGCA	2970
rs362304	10220	GCACAGAUGCCAUGGCAUG	1219	10220	GCACAGAUGCCAUGGCAUG	1219	10238	CAUGCCAUGGCAUCUGUGC	2971
rs362304	10221	CACAGAUGCCAUGGCAUGU	1220	10221	CACAGAUGCCAUGGCAUGU	1220	10239	ACAUGCCAUGGCAUCUGUG	2972
rs362304	10222	ACAGAUGCCAUGGCAUGUG	1221	10222	ACAGAUGCCAUGGCAUGUG	1221	10240	CACAUGCCAUGGCAUCUGU	2973
rs362304	10223	CAGAUGCCAUGGCAUGUGC	1222	10223	CAGAUGCCAUGGCAUGUGC	1222	10241	GCACAUGCCAUGGCAUCUG	2974
rs362304	10224	AGAUGCCAUGGCAUGUGCU	1223	10224	AGAUGCCAUGGCAUGUGCU	1223	10242	AGACAUGCCAUGGCAUCU	2975
rs362304	10225	GAUGCCAUGGCAUGUGCUG	1224	10225	GAUGCCAUGGCAUGUGCUG	1224	10243	CAGACAUGCCAUGGCAUC	2976
rs362304	10226	AUGCCAUGGCAUGUGCUGG	1225	10226	AUGCCAUGGCAUGUGCUGG	1225	10244	CCAGACAUGCCAUGGCAU	2977
rs362304	10227	UGCCAUGGCAUGUGCUGGG	1226	10227	UGCCAUGGCAUGUGCUGGG	1226	10245	CCAGACAUGCCAUGGCA	2978
rs362304	10228	GCCAUGGCAUGUGCUGGGC	1227	10228	GCCAUGGCAUGUGCUGGGC	1227	10246	GCCAGACAUGGCCAUGGC	2979
rs362304	10229	CCAUGGCAUGUGCUGGGCC	1228	10229	CCAUGGCAUGUGCUGGGCC	1228	10247	GGCCAGACAUGGCCAUGG	2980
rs362304	10230	CAUGGCAUGUGCUGGGCCA	1229	10230	CAUGGCAUGUGCUGGGCCA	1229	10248	UGGCCAGACAUGGCCAUG	2981
rs362304	10231	AUGGCAUGUGCUGGGCCAG	1230	10231	AUGGCAUGUGCUGGGCCAG	1230	10249	CUGGCCAGACAUGGCCAU	2982
rs362304	10232	UGGCAUGUGCUGGGCCAGU	1231	10232	UGGCAUGUGCUGGGCCAGU	1231	10250	ACUGGCCAGACAUGGCCA	2983
rs362304	10233	GGCAUGUGCUGGGCCAGUG	1232	10233	GGCAUGUGCUGGGCCAGUG	1232	10251	CACUGGCCAGACAUGGCC	2984
rs362304	10234	GCAUGUGCUGGGCCAGUGG	1233	10234	GCAUGUGCUGGGCCAGUGG	1233	10252	CCACUGGCCAGACAUGC	2985
rs362304	10235	CAUGUGCUGGGCCAGUGGC	1234	10235	CAUGUGCUGGGCCAGUGGC	1234	10253	GCCACUGGCCAGACAUG	2986
rs362304	10236	AUGUGCUGGGCCAGUGGCU	1235	10236	AUGUGCUGGGCCAGUGGCU	1235	10254	AGCCACUGGCCAGACAUG	2987
rs362303	10253	CUGGGGUGCUAGACACCC	1236	10253	CUGGGGUGCUAGACACCC	1236	10271	GGGUGUCUAGCACCCCCAG	2988
rs362303	10254	UGGGGUGCUAGACACCCG	1237	10254	UGGGGUGCUAGACACCCG	1237	10272	CGGGUGUCUAGCACCCCCA	2989
rs362303	10255	GGGGUGCUAGACACCCGG	1238	10255	GGGGUGCUAGACACCCGG	1238	10273	CCGGGUGUCUAGCACCCCC	2990
rs362303	10256	GGGGUGCUAGACACCCGGC	1239	10256	GGGGUGCUAGACACCCGGC	1239	10274	GCCGGGUGUCUAGCACCCC	2991
rs362303	10257	GGGUGCUAGACACCCGGCA	1240	10257	GGGUGCUAGACACCCGGCA	1240	10275	UGCCGGGUGUCUAGCACCC	2992
rs362303	10258	GGUGCUAGACACCCGGCAC	1241	10258	GGUGCUAGACACCCGGCAC	1241	10276	GUGCCGGGUGUCUAGCAC	2993
rs362303	10259	GUGCUAGACACCCGGCAC	1242	10259	GUGCUAGACACCCGGCAC	1242	10277	GGUGCCGGGUGUCUAGCAC	2994
rs362303	10260	UGCUAGACACCCGGCACCA	1243	10260	UGCUAGACACCCGGCACCA	1243	10278	UGGUGCCGGGUGUCUAGCA	2995
rs362303	10261	GCUAGACACCCGGCACCAU	1244	10261	GCUAGACACCCGGCACCAU	1244	10279	AUGGUGCCGGGUGUCUAGC	2996

rs362303	10262	CUAGACACCCGGCACCAUUC	1245	10262	CUAGACACCCGGCACCAUUC	1245	10280	AUUGGUGCCGGGUGUCUAG	2997
rs362303	10263	UAGACACCCGGCACCAUUC	1246	10263	UAGACACCCGGCACCAUUC	1246	10281	GAUUGGUGCCGGGUGUCUA	2998
rs362303	10264	AGACACCCGGCACCAUUCU	1247	10264	AGACACCCGGCACCAUUCU	1247	10282	AGAAUGGUGCCGGGUGUCU	2999
rs362303	10265	GACACCCGGCACCAUUCUC	1248	10265	GACACCCGGCACCAUUCUC	1248	10283	GAGAAUGGUGCCGGGUGUC	3000
rs362303	10266	ACACCCGGCACCAUUCUCC	1249	10266	ACACCCGGCACCAUUCUCC	1249	10284	GGAGAAUGGUGCCGGGUGU	3001
rs362303	10267	CACCCGGCACCAUUCUCCC	1250	10267	CACCCGGCACCAUUCUCCC	1250	10285	GGGAGAAUGGUGCCGGGUG	3002
rs362303	10268	ACCCGGCACCAUUCUCCCU	1251	10268	ACCCGGCACCAUUCUCCCU	1251	10286	AGGGAGAAUGGUGCCGGGU	3003
rs362303	10269	CCGGCACCAUUCUCCCUU	1252	10269	CCGGCACCAUUCUCCCUU	1252	10287	AAGGGAGAAUGGUGCCGGG	3004
rs362303	10270	CGGGCACCAUUCUCCUUC	1253	10270	CGGGCACCAUUCUCCUUC	1253	10288	GAAGGGAGAAUGGUGCCGG	3005
rs362303	10271	CUGGCACCAUUCUCCUUCU	1254	10271	CUGGCACCAUUCUCCUUCU	1254	10289	AGAAGGGAGAAUGGUGCCG	3006
rs362303	10253	CUGGGGGUGCUAGACACCU	1255	10253	CUGGGGUGCUAGACACCU	1255	10271	AGGUGUCUAGCACCCCCAG	3007
rs362303	10254	UGGGGGGUGCUAGACACCU	1256	10254	UGGGGGGUGCUAGACACCU	1256	10272	CAGGUGUCUAGCACCCCCA	3008
rs362303	10255	GGGGGUGCUAGACACCUUG	1257	10255	GGGGGUGCUAGACACCUUG	1257	10273	CCAGGUGUCUAGCACCCCC	3009
rs362303	10256	GGGGGUGCUAGACACCUUGC	1258	10256	GGGGGUGCUAGACACCUUGC	1258	10274	GCCAGGUGUCUAGCACCC	3010
rs362303	10257	GGGUGCUAGACACCUUGCA	1259	10257	GGGUGCUAGACACCUUGCA	1259	10275	UGCCAGGUGUCUAGCACCC	3011
rs362303	10258	GGGUGCUAGACACCUUGGC	1260	10258	GGGUGCUAGACACCUUGGC	1260	10276	GUGCCAGGUGUCUAGCAC	3012
rs362303	10259	GUGCUAGACACCUUGGCACC	1261	10259	GUGCUAGACACCUUGGCACC	1261	10277	GGUGCCAGGUGUCUAGCAC	3013
rs362303	10260	UGCUAGACACCUUGGCACCA	1262	10260	UGCUAGACACCUUGGCACCA	1262	10278	UGGUGCCAGGUGUCUAGCA	3014
rs362303	10261	GCUAGACACCUUGGCACCAU	1263	10261	GCUAGACACCUUGGCACCAU	1263	10279	AUGGUGCCAGGUGUCUAGC	3015
rs362303	10262	CUAGACACCUUGGCACCAUUC	1264	10262	CUAGACACCUUGGCACCAUUC	1264	10280	AUUGGUGCCAGGUGUCUAG	3016
rs362303	10263	UAGACACCUUGGCACCAUUC	1265	10263	UAGACACCUUGGCACCAUUC	1265	10281	GAUUGGUGCCAGGUGUCUA	3017
rs362303	10264	AGACACCUUGGCACCAUUCU	1266	10264	AGACACCUUGGCACCAUUCU	1266	10282	AGAAUGGUGCCAGGUGUCU	3018
rs362303	10265	GACACCUUGGCACCAUUCUC	1267	10265	GACACCUUGGCACCAUUCUC	1267	10283	GAGAAUGGUGCCAGGUGUC	3019
rs362303	10266	ACACCUUGGCACCAUUCUCC	1268	10266	ACACCUUGGCACCAUUCUCC	1268	10284	GGAGAAUGGUGCCAGGUGU	3020
rs362303	10267	CACCUUGGCACCAUUCUCCC	1269	10267	CACCUUGGCACCAUUCUCCC	1269	10285	GGGAGAAUGGUGCCAGGUG	3021
rs362303	10268	ACCUGGCACCAUUCUCCCU	1270	10268	ACCUGGCACCAUUCUCCCU	1270	10286	AGGGAGAAUGGUGCCAGG	3022
rs362303	10269	CCUGGCACCAUUCUCCCUU	1271	10269	CCUGGCACCAUUCUCCCUU	1271	10287	AAGGGAGAAUGGUGCCAGG	3023
rs362303	10270	CUGGCACCAUUCUCCCUUC	1272	10270	CUGGCACCAUUCUCCCUUC	1272	10288	GAAGGGAGAAUGGUGCCAG	3024
rs362303	10271	UGGCACCAUUCUCCCUUCU	1273	10271	UGGCACCAUUCUCCCUUCU	1273	10289	AGAAGGGAGAAUGGUGCCA	3025
rs1557210	10861	UGUGUUUGUCUGAGCCUC	1274	10861	UGUGUUUGUCUGAGCCUC	1274	10879	GAGGUCUCAGACAAAACACA	3026
rs1557210	10862	GUGUUUGUCUGAGCCUCU	1275	10862	GUGUUUGUCUGAGCCUCU	1275	10880	AGAGGUCUCAGACAAAACAC	3027
rs1557210	10863	UGUUUGUCUGAGCCUCUC	1276	10863	UGUUUGUCUGAGCCUCUC	1276	10881	GAGAGGUCUCAGACAAAAC	3028
rs1557210	10864	GUUUUGUCUGAGCCUCUCU	1277	10864	GUUUUGUCUGAGCCUCUCU	1277	10882	AGAGAGGUCUCAGACAAAAC	3029
rs1557210	10865	UUUUUGUCUGAGCCUCUCUC	1278	10865	UUUUUGUCUGAGCCUCUCUC	1278	10883	GAGAGAGGUCUCAGACAAA	3030
rs1557210	10866	UUUGUCUGAGCCUCUCUCG	1279	10866	UUUGUCUGAGCCUCUCUCG	1279	10884	CGAGAGAGGUCUCAGACAAA	3031
rs1557210	10867	UUGUCUGAGCCUCUCUCGG	1280	10867	UUGUCUGAGCCUCUCUCGG	1280	10885	CCGAGAGAGGUCUCAGACAA	3032
rs1557210	10868	UGUCUGAGCCUCUCUCGGU	1281	10868	UGUCUGAGCCUCUCUCGGU	1281	10886	ACCGAGAGAGGUCUCAGACA	3033
rs1557210	10869	GUCUGAGCCUCUCUCGGUC	1282	10869	GUCUGAGCCUCUCUCGGUC	1282	10887	GACCGAGAGAGGUCUCAGAC	3034
rs1557210	10870	UCUGAGCCUCUCUCGGUCA	1283	10870	UCUGAGCCUCUCUCGGUCA	1283	10888	UGACCGAGAGAGGUCUCAGA	3035

rs1557210	10871	CUGAGCCUCUCUCGGUCAAC	1284	10871	CUGAGCCUCUCUCGGUCAAC	1284	10889	UUGACCGAGAGAGGCUACG	3036
rs1557210	10872	UGAGCCUCUCUCGGUCAAC	1285	10872	UGAGCCUCUCUCGGUCAAC	1285	10890	GUUGACCGAGAGAGGCUAC	3037
rs1557210	10873	GAGCCUCUCUCGGUCAACA	1286	10873	GAGCCUCUCUCGGUCAACA	1286	10891	UGUUGACCGAGAGAGGCU	3038
rs1557210	10874	AGCCUCUCUCGGUCAACAG	1287	10874	AGCCUCUCUCGGUCAACAG	1287	10892	CUGUUGACCGAGAGAGGCU	3039
rs1557210	10875	GCCUCUCUCGGUCAACAGC	1288	10875	GCCUCUCUCGGUCAACAGC	1288	10893	GCUGUUGACCGAGAGAGGC	3040
rs1557210	10876	CCUCUCUCGGUCAACAGCA	1289	10876	CCUCUCUCGGUCAACAGCA	1289	10894	UGCUGUUGACCGAGAGAGG	3041
rs1557210	10877	CUCUCUCGGUCAACAGCAA	1290	10877	CUCUCUCGGUCAACAGCAA	1290	10895	UUGCUGUUGACCGAGAGAG	3042
rs1557210	10878	UCUCUCGGUCAACAGCAAA	1291	10878	UCUCUCGGUCAACAGCAAA	1291	10896	UUUGCUGUUGACCGAGAGAG	3043
rs1557210	10879	CUCUCGGUCAACAGCAAAG	1292	10879	CUCUCGGUCAACAGCAAAG	1292	10897	CUUUGCUGUUGACCGAGAG	3044
rs1557210	10861	UGUGUUUUGUCUGAGCCUU	1293	10861	UGUGUUUUGUCUGAGCCUU	1293	10879	AAGGCUACAGACAAAACACA	3045
rs1557210	10862	GUGUUUUGUCUGAGCCUUU	1294	10862	GUGUUUUGUCUGAGCCUUU	1294	10880	AAAGGCUACAGACAAAACAC	3046
rs1557210	10863	UGUUUUGUCUGAGCCUUUC	1295	10863	UGUUUUGUCUGAGCCUUUC	1295	10881	GAAAGGCUACAGACAAAACA	3047
rs1557210	10864	GUUUUGUCUGAGCCUUUCU	1296	10864	GUUUUGUCUGAGCCUUUCU	1296	10882	AGAAAGGCUACAGACAAAAC	3048
rs362302	10880	UCUCGGUCAACAGCAAAGC	1297	10880	UCUCGGUCAACAGCAAAGC	1297	10898	GCUUUGCUGUUGACCCGAGA	3049
rs362302	10881	CUCGGUCAACAGCAAAGCU	1298	10881	CUCGGUCAACAGCAAAGCU	1298	10899	AGCUUUGCUGUUGACCCGAG	3050
rs362302	10882	UCGGUCAACAGCAAAGCUU	1299	10882	UCGGUCAACAGCAAAGCUU	1299	10900	AAGCUUUGCUGUUGACCCGA	3051
rs362302	10883	CGGUCAACAGCAAAGCUUG	1300	10883	CGGUCAACAGCAAAGCUUG	1300	10901	CAAGCUUUGCUGUUGACCCG	3052
rs362302	10865	UUUUGUCUGAGCCUCUCUU	1301	10865	UUUUGUCUGAGCCUCUCUU	1301	10883	AAGAGAGGCUACAGACAAA	3053
rs362302	10866	UUUGUCUGAGCCUCUCUUUG	1302	10866	UUUGUCUGAGCCUCUCUUUG	1302	10884	CAAGAGAGGCUACAGACAAA	3054
rs362302	10867	UUGUCUGAGCCUCUCUUUGG	1303	10867	UUGUCUGAGCCUCUCUUUGG	1303	10885	CCAAGAGAGGCUACAGACAA	3055
rs362302	10868	UGUCUGAGCCUCUCUUUGGU	1304	10868	UGUCUGAGCCUCUCUUUGGU	1304	10886	ACCAAGAGAGGCUACAGACA	3056
rs362302	10869	GUCUGAGCCUCUCUUUGGUC	1305	10869	GUCUGAGCCUCUCUUUGGUC	1305	10887	GACCAAGAGAGGCUACAGAC	3057
rs362302	10870	UCUGAGCCUCUCUUUGGUCA	1306	10870	UCUGAGCCUCUCUUUGGUCA	1306	10888	UGACCAAGAGAGGCUACAGA	3058
rs362302	10871	CUGAGCCUCUCUUUGGUCAA	1307	10871	CUGAGCCUCUCUUUGGUCAA	1307	10889	UUGACCAAGAGAGGCUACAG	3059
rs362302	10872	UGAGCCUCUCUUUGGUCAAC	1308	10872	UGAGCCUCUCUUUGGUCAAC	1308	10890	GUUGACCAAGAGAGGCUCA	3060
rs362302	10873	GAGCCUCUCUUUGGUCAACA	1309	10873	GAGCCUCUCUUUGGUCAACA	1309	10891	UGUUGACCAAGAGAGGCU	3061
rs362302	10874	AGCCUCUCUUUGGUCAACAG	1310	10874	AGCCUCUCUUUGGUCAACAG	1310	10892	CUGUUGACCAAGAGAGGCU	3062
rs362302	10875	GCCUCUCUUUGGUCAACAGC	1311	10875	GCCUCUCUUUGGUCAACAGC	1311	10893	GCUGUUGACCAAGAGAGGC	3063
rs362302	10876	CCUCUCUUUGGUCAACAGCA	1312	10876	CCUCUCUUUGGUCAACAGCA	1312	10894	UGCUGUUGACCAAGAGAGG	3064
rs362302	10877	CUCUCUUUGGUCAACAGCAA	1313	10877	CUCUCUUUGGUCAACAGCAA	1313	10895	UUGCUGUUGACCAAGAGAG	3065
rs362302	10878	UCUCUUUGGUCAACAGCAAA	1314	10878	UCUCUUUGGUCAACAGCAAA	1314	10896	UUUGCUGUUGACCAAGAGAGA	3066
rs362302	10879	CUCUUGGUCAACAGCAAAG	1315	10879	CUCUUGGUCAACAGCAAAG	1315	10897	CUUUGCUGUUGACCAAGAG	3067
rs362302	10880	UCUUGGUCAACAGCAAAGC	1316	10880	UCUUGGUCAACAGCAAAGC	1316	10898	GCUUUGCUGUUGACCAAGA	3068
rs362302	10881	CUUGGUCAACAGCAAAGCU	1317	10881	CUUGGUCAACAGCAAAGCU	1317	10899	AGCUUUGCUGUUGACCAAG	3069
rs362302	10882	UUGGUCAACAGCAAAGCUU	1318	10882	UUGGUCAACAGCAAAGCUU	1318	10900	AAGCUUUGCUGUUGACCAAA	3070
rs362302	10883	UGGUCAACAGCAAAGCUUG	1319	10883	UGGUCAACAGCAAAGCUUG	1319	10901	CAAGCUUUGCUGUUGACCA	3071
rs3025805	10953	CAGCUGACAUCUUGCACGG	1320	10953	CAGCUGACAUCUUGCACGG	1320	10971	CCGUGCAAGAUGUCAGCUG	3072
rs3025805	10954	AGCUGACAUCUUGCACGGU	1321	10954	AGCUGACAUCUUGCACGGU	1321	10972	ACCGUGCAAGAUGUCAGCU	3073
rs3025805	10955	GCUGACAUCUUGCACGGUG	1322	10955	GCUGACAUCUUGCACGGUG	1322	10973	CACCGUGCAAGAUGUCAGC	3074

rs3025805	10956	CUGACAUCUUGCACGGUGA	1323	10956	CUGACAUCUUGCACGGUGA	1323	10974	UCACCGUGCAAGAUGUCAG	3075
rs3025805	10957	UGACAUCUUGCACGGUGAC	1324	10957	UGACAUCUUGCACGGUGAC	1324	10975	GUCACCGUGCAAGAUGUCA	3076
rs3025805	10958	GACAUCUUGCACGGUGACC	1325	10958	GACAUCUUGCACGGUGACC	1325	10976	GGUCACCGUGCAAGAUGUC	3077
rs3025805	10959	ACAUCUUGCACGGUGACCC	1326	10959	ACAUCUUGCACGGUGACCC	1326	10977	GGGUCACCGUGCAAGAUGU	3078
rs3025805	10960	CAUCUUGCACGGUGACCCC	1327	10960	CAUCUUGCACGGUGACCCC	1327	10978	GGGGUCACCGUGCAAGAUG	3079
rs3025805	10961	AUCUUGCACGGUGACCCCU	1328	10961	AUCUUGCACGGUGACCCCU	1328	10979	AGGGGUCACCGUGCAAGAU	3080
rs3025805	10962	UCUUGCACGGUGACCCCUU	1329	10962	UCUUGCACGGUGACCCCUU	1329	10980	AAGGGGUCACCGUGCAAGA	3081
rs3025805	10963	CUUGCACGGUGACCCCUUU	1330	10963	CUUGCACGGUGACCCCUUU	1330	10981	AAAGGGGUCACCGUGCAAG	3082
rs3025805	10964	UUGCACGGUGACCCCUUUU	1331	10964	UUGCACGGUGACCCCUUUU	1331	10982	AAAAGGGGUCACCGUGCAA	3083
rs3025805	10965	UGCACGGUGACCCCUUUUA	1332	10965	UGCACGGUGACCCCUUUUA	1332	10983	UAAAAGGGGUCACCGUGCA	3084
rs3025805	10966	GCACGGUGACCCCUUUUAG	1333	10966	GCACGGUGACCCCUUUUAG	1333	10984	CUAAAAGGGGUCACCGUGC	3085
rs3025805	10967	CACGGUGACCCCUUUUAGU	1334	10967	CACGGUGACCCCUUUUAGU	1334	10985	ACUAAAAGGGGUCACCGUG	3086
rs3025805	10968	ACGGUGACCCCUUUUAGUC	1335	10968	ACGGUGACCCCUUUUAGUC	1335	10986	GACUAAAAGGGGUCACCGU	3087
rs3025805	10969	CGGUGACCCCUUUUAGUCA	1336	10969	CGGUGACCCCUUUUAGUCA	1336	10987	UGACUAAAAGGGGUCACCG	3088
rs3025805	10970	GGUGACCCCUUUUAGUCAG	1337	10970	GGUGACCCCUUUUAGUCAG	1337	10988	CUGACUAAAAGGGGUCACC	3089
rs3025805	10971	GUGACCCCUUUUAGUCAGG	1338	10971	GUGACCCCUUUUAGUCAGG	1338	10989	CCUGACUAAAAGGGGUCAC	3090
rs3025805	10953	CAGCUGACAUCUUGCACGU	1339	10953	CAGCUGACAUCUUGCACGU	1339	10971	ACGUGCAAGAUGUCAGCUG	3091
rs3025805	10954	AGCUGACAUCUUGCACGUU	1340	10954	AGCUGACAUCUUGCACGUU	1340	10972	AACGUGCAAGAUGUCAGCU	3092
rs3025805	10955	GCUGACAUCUUGCACGUUG	1341	10955	GCUGACAUCUUGCACGUUG	1341	10973	CAACGUGCAAGAUGUCAGC	3093
rs3025805	10956	CUGACAUCUUGCACGUUGA	1342	10956	CUGACAUCUUGCACGUUGA	1342	10974	UCAACGUGCAAGAUGUCAG	3094
rs3025805	10957	UGACAUCUUGCACGUUGAC	1343	10957	UGACAUCUUGCACGUUGAC	1343	10975	GUCAACGUGCAAGAUGUCA	3095
rs3025805	10958	GACAUCUUGCACGUUGACC	1344	10958	GACAUCUUGCACGUUGACC	1344	10976	GGUCAACGUGCAAGAUGUC	3096
rs3025805	10959	ACAUCUUGCACGUUGACCC	1345	10959	ACAUCUUGCACGUUGACCC	1345	10977	GGGUCAACGUGCAAGAUGU	3097
rs3025805	10960	CAUCUUGCACGUUGACCCC	1346	10960	CAUCUUGCACGUUGACCCC	1346	10978	GGGGUCAACGUGCAAGAUG	3098
rs3025805	10961	AUCUUGCACGUUGACCCCU	1347	10961	AUCUUGCACGUUGACCCCU	1347	10979	AGGGGUCAACGUGCAAGAU	3099
rs3025805	10962	UCUUGCACGUUGACCCCUU	1348	10962	UCUUGCACGUUGACCCCUU	1348	10980	AAGGGGUCAACGUGCAAGA	3100
rs3025805	10963	CUUGCACGUUGACCCCUUU	1349	10963	CUUGCACGUUGACCCCUUU	1349	10981	AAAGGGGUCAACGUGCAAG	3101
rs3025805	10964	UUGCACGUUGACCCCUUUU	1350	10964	UUGCACGUUGACCCCUUUU	1350	10982	AAAAGGGGUCAACGUGCAA	3102
rs3025805	10965	UGCACGUUGACCCCUUUUA	1351	10965	UGCACGUUGACCCCUUUUA	1351	10983	UAAAAGGGGUCAACGUGCA	3103
rs3025805	10966	GCACGUUGACCCCUUUUAG	1352	10966	GCACGUUGACCCCUUUUAG	1352	10984	CUAAAAGGGGUCAACGUGC	3104
rs3025805	10967	CACGUUGACCCCUUUUAGU	1353	10967	CACGUUGACCCCUUUUAGU	1353	10985	ACUAAAAGGGGUCAACGUG	3105
rs3025805	10968	ACGUUGACCCCUUUUAGUC	1354	10968	ACGUUGACCCCUUUUAGUC	1354	10986	GACUAAAAGGGGUCAACGU	3106
rs3025805	10969	CGUUGACCCCUUUUAGUCA	1355	10969	CGUUGACCCCUUUUAGUCA	1355	10987	UGACUAAAAGGGGUCAACG	3107
rs3025805	10970	GUUGACCCCUUUUAGUCAG	1356	10970	GUUGACCCCUUUUAGUCAG	1356	10988	CUGACUAAAAGGGGUCAAC	3108
rs3025805	10971	UUGACCCCUUUUAGUCAGG	1357	10971	UUGACCCCUUUUAGUCAGG	1357	10989	CCUGACUAAAAGGGGUCAA	3109
rs362267	11163	UUUGGAGCUCUGCUUGCC	1358	11163	UUUGGAGCUCUGCUUGCC	1358	11181	GGCAAGCAGAGCUCCCAA	3110
rs362267	11164	UUGGAGCUCUGCUUGCCG	1359	11164	UUGGAGCUCUGCUUGCCG	1359	11182	CGGCAAGCAGAGCUCCCAA	3111
rs362267	11165	UGGAGCUCUGCUUGCCGA	1360	11165	UGGAGCUCUGCUUGCCGA	1360	11183	UCGGCAAGCAGAGCUCCCA	3112
rs362267	11166	GGGAGCUCUGCUUGCCGAC	1361	11166	GGGAGCUCUGCUUGCCGAC	1361	11184	GUCGGCAAGCAGAGCUCCC	3113

rs362267	11167	GGAGCUCUGCUUGCCGACU	1362	11167	GGAGCUCUGCUUGCCGACU	1362	11185	AGUCGGCAAGCAGAGCUCC	3114
rs362267	11168	GAGCUCUGCUUGCCGACUG	1363	11168	GAGCUCUGCUUGCCGACUG	1363	11186	CAGUCGGCAAGCAGAGCUC	3115
rs362267	11169	AGCUCUGCUUGCCGACUGG	1364	11169	AGCUCUGCUUGCCGACUGG	1364	11187	CCAGUCGGCAAGCAGAGCU	3116
rs362267	11170	GCUCUGCUUGCCGACUGGC	1365	11170	GCUCUGCUUGCCGACUGGC	1365	11188	GCCAGUCGGCAAGCAGAGC	3117
rs362267	11171	CUCUGCUUGCCGACUGGCU	1366	11171	CUCUGCUUGCCGACUGGCU	1366	11189	AGCCAGUCGGCAAGCAGAG	3118
rs362267	11172	UCUGCUUGCCGACUGGCU	1367	11172	UCUGCUUGCCGACUGGCU	1367	11190	CAGCCAGUCGGCAAGCAGA	3119
rs362267	11173	CUGCUUGCCGACUGGCU	1368	11173	CUGCUUGCCGACUGGCU	1368	11191	ACAGCCAGUCGGCAAGCAG	3120
rs362267	11174	UGCUUGCCGACUGGCUUG	1369	11174	UGCUUGCCGACUGGCUUG	1369	11192	CACAGCCAGUCGGCAAGCA	3121
rs362267	11175	GCUUGCCGACUGGCUUGA	1370	11175	GCUUGCCGACUGGCUUGA	1370	11193	UCACAGCCAGUCGGCAAGC	3122
rs362267	11176	CUUGCCGACUGGCUUGAG	1371	11176	CUUGCCGACUGGCUUGAG	1371	11194	UCACAGCCAGUCGGCAAG	3123
rs362267	11177	UUGCCGACUGGCUUGAGAG	1372	11177	UUGCCGACUGGCUUGAGAG	1372	11195	UCUCACAGCCAGUCGGCAA	3124
rs362267	11178	UGCCGACUGGCUUGAGAC	1373	11178	UGCCGACUGGCUUGAGAC	1373	11196	GUCUCACAGCCAGUCGGCA	3125
rs362267	11179	GCCGACUGGCUUGAGACG	1374	11179	GCCGACUGGCUUGAGACG	1374	11197	CGUCUCACAGCCAGUCGGC	3126
rs362267	11180	CCGACUGGCUUGAGACGA	1375	11180	CCGACUGGCUUGAGACGA	1375	11198	UCGUCUCACAGCCAGUCGG	3127
rs362267	11181	CGACUGGCUUGAGACGAG	1376	11181	CGACUGGCUUGAGACGAG	1376	11199	CUCGUCUCACAGCCAGUCG	3128
rs362267	11163	UUUGGAGCUCUGCUUGCU	1377	11163	UUUGGAGCUCUGCUUGCU	1377	11181	AGCAAGCAGAGCUCUCCAAA	3129
rs362267	11164	UUGGAGCUCUGCUUGCUG	1378	11164	UUGGAGCUCUGCUUGCUG	1378	11182	CAGCAAGCAGAGCUCUCCAA	3130
rs362267	11165	UGGAGCUCUGCUUGCUGA	1379	11165	UGGAGCUCUGCUUGCUGA	1379	11183	UCAGCAAGCAGAGCUCUCCA	3131
rs362267	11166	GGGAGCUCUGCUUGCUGAC	1380	11166	GGGAGCUCUGCUUGCUGAC	1380	11184	GUCAGCAAGCAGAGCUCUCC	3132
rs362267	11167	GGAGCUCUGCUUGCUGACU	1381	11167	GGAGCUCUGCUUGCUGACU	1381	11185	AGUCAGCAAGCAGAGCUCUCC	3133
rs362267	11168	GAGCUCUGCUUGCUGACUG	1382	11168	GAGCUCUGCUUGCUGACUG	1382	11186	CAGUCAGCAAGCAGAGCUCU	3134
rs362267	11169	AGCUCUGCUUGCUGACUGG	1383	11169	AGCUCUGCUUGCUGACUGG	1383	11187	CCAGUCAGCAAGCAGAGCUCU	3135
rs362267	11170	GCUCUGCUUGCUGACUGGC	1384	11170	GCUCUGCUUGCUGACUGGC	1384	11188	GCCAGUCAGCAAGCAGAGC	3136
rs362267	11171	CUCUGCUUGCUGACUGGCU	1385	11171	CUCUGCUUGCUGACUGGCU	1385	11189	AGCCAGUCAGCAAGCAGAG	3137
rs362267	11172	UCUGCUUGCUGACUGGCU	1386	11172	UCUGCUUGCUGACUGGCU	1386	11190	CAGCCAGUCAGCAAGCAGA	3138
rs362267	11173	CUGCUUGCUGACUGGCU	1387	11173	CUGCUUGCUGACUGGCU	1387	11191	ACAGCCAGUCAGCAAGCAG	3139
rs362267	11174	UGCUUGCUGACUGGCUUG	1388	11174	UGCUUGCUGACUGGCUUG	1388	11192	CACAGCCAGUCAGCAAGCA	3140
rs362267	11175	GCUUGCUGACUGGCUUGA	1389	11175	GCUUGCUGACUGGCUUGA	1389	11193	UCACAGCCAGUCAGCAAGC	3141
rs362267	11176	CUUGCUGACUGGCUUGAG	1390	11176	CUUGCUGACUGGCUUGAG	1390	11194	UCACAGCCAGUCAGCAAG	3142
rs362267	11177	UUGCUGACUGGCUUGAGAG	1391	11177	UUGCUGACUGGCUUGAGAG	1391	11195	UCUCACAGCCAGUCAGCA	3143
rs362267	11178	UGCUGACUGGCUUGAGAC	1392	11178	UGCUGACUGGCUUGAGAC	1392	11196	GUCUCACAGCCAGUCAGCA	3144
rs362267	11179	GCUGACUGGCUUGAGACG	1393	11179	GCUGACUGGCUUGAGACG	1393	11197	CGUCUCACAGCCAGUCAGC	3145
rs362267	11180	CUGACUGGCUUGAGACGA	1394	11180	CUGACUGGCUUGAGACGA	1394	11198	UCGUCUCACAGCCAGUCAG	3146
rs362267	11181	UGACUGGCUUGAGACGAG	1395	11181	UGACUGGCUUGAGACGAG	1395	11199	CUCGUCUCACAGCCAGUCA	3147
rs362301	11382	UGGAGCUGGGGAGCAGCU	1396	11382	UGGAGCUGGGGAGCAGCU	1396	11400	AGCUGCUCCCCAGCUGCCA	3148
rs362301	11383	GGCAGCUGGGGAGCAGCUG	1397	11383	GGCAGCUGGGGAGCAGCUG	1397	11401	CAGCUGCUCCCCAGCUGCC	3149
rs362301	11384	GCAGCUGGGGAGCAGCUGA	1398	11384	GCAGCUGGGGAGCAGCUGA	1398	11402	UCAGCUGCUCCCCAGCUGC	3150
rs362301	11385	CAGCUGGGGAGCAGCUGAG	1399	11385	CAGCUGGGGAGCAGCUGAG	1399	11403	CUCAGCUGCUCCCCAGCUG	3151
rs362301	11386	AGCUGGGGAGCAGCUGAGA	1400	11386	AGCUGGGGAGCAGCUGAGA	1400	11404	UCUCAGCUGCUCCCCAGCU	3152

rs362301	11387	GCUGGGGAGCAGCUGAGAU	1401	11387	GCUGGGGAGCAGCUGAGAU	1401	11405	AUCUCAGCUGCUCCCCAGC	3153
rs362301	11388	CUGGGGAGCAGCUGAGAU	1402	11388	CUGGGGAGCAGCUGAGAU	1402	11406	CAUCUCAGCUGCUCCCCAG	3154
rs362301	11389	UGGGGAGCAGCUGAGAU	1403	11389	UGGGGAGCAGCUGAGAU	1403	11407	ACAUCUCAGCUGCUCCCCA	3155
rs362301	11390	GGGAGCAGCUGAGAU	1404	11390	GGGAGCAGCUGAGAU	1404	11408	CACAUCUCAGCUGCUCCCC	3156
rs362301	11391	GGGAGCAGCUGAGAU	1405	11391	GGGAGCAGCUGAGAU	1405	11409	CCACAUCUCAGCUGCUCCC	3157
rs362301	11392	GGGAGCAGCUGAGAU	1406	11392	GGGAGCAGCUGAGAU	1406	11410	UCCACAUCUCAGCUGCUCC	3158
rs362301	11393	GAGCAGCUGAGAU	1407	11393	GAGCAGCUGAGAU	1407	11411	GUCCACAUCUCAGCUGCUC	3159
rs362301	11394	AGCAGCUGAGAU	1408	11394	AGCAGCUGAGAU	1408	11412	AGUCCACAUCUCAGCUGCU	3160
rs362301	11395	GCAGCUGAGAU	1409	11395	GCAGCUGAGAU	1409	11413	AAGUCCACAUCUCAGCUGC	3161
rs362301	11396	CAGCUGAGAU	1410	11396	CAGCUGAGAU	1410	11414	CAAGUCCACAUCUCAGCUG	3162
rs362301	11397	AGCUGAGAU	1411	11397	AGCUGAGAU	1411	11415	ACAAGUCCACAUCUCAGCU	3163
rs362301	11398	GCUGAGAU	1412	11398	GCUGAGAU	1412	11416	UACAAGUCCACAUCUCAGC	3164
rs362301	11399	CUGAGAU	1413	11399	CUGAGAU	1413	11417	AUACAAGUCCACAUCUCAG	3165
rs362301	11400	UGAGAU	1414	11400	UGAGAU	1414	11418	CAUACAAGUCCACAUCUCA	3166
rs362301	11382	UGGAGCUGGGAGCAGCG	1415	11382	UGGAGCUGGGAGCAGCG	1415	11400	CGCUGCUCCCCAGCUGCCA	3167
rs362301	11383	GGCAGCUGGGAGCAGCGG	1416	11383	GGCAGCUGGGAGCAGCGG	1416	11401	CCGCUGCUCCCCAGCUGCC	3168
rs362301	11384	GCAGCUGGGAGCAGCGGA	1417	11384	GCAGCUGGGAGCAGCGGA	1417	11402	UCCGCUGCUCCCCAGCUGC	3169
rs362301	11385	CAGCUGGGAGCAGCGGAG	1418	11385	CAGCUGGGAGCAGCGGAG	1418	11403	CUCCGCUGCUCCCCAGCUG	3170
rs362301	11386	AGCUGGGAGCAGCGGAGA	1419	11386	AGCUGGGAGCAGCGGAGA	1419	11404	UCUCCGCUGCUCCCCAGCU	3171
rs362301	11387	GCUGGGAGCAGCGGAGAU	1420	11387	GCUGGGAGCAGCGGAGAU	1420	11405	AUCUCCGCUGCUCCCCAGC	3172
rs362301	11388	CUGGGAGCAGCGGAGAU	1421	11388	CUGGGAGCAGCGGAGAU	1421	11406	CAUCUCCGCUGCUCCCCAG	3173
rs362301	11389	UGGGAGCAGCGGAGAU	1422	11389	UGGGAGCAGCGGAGAU	1422	11407	ACAUCUCCGCUGCUCCCCA	3174
rs362301	11390	GGGAGCAGCGGAGAU	1423	11390	GGGAGCAGCGGAGAU	1423	11408	CACAUCUCCGCUGCUCCCC	3175
rs362301	11391	GGGAGCAGCGGAGAU	1424	11391	GGGAGCAGCGGAGAU	1424	11409	CCACAUCUCCGCUGCUCCC	3176
rs362301	11392	GGAGCAGCGGAGAU	1425	11392	GGAGCAGCGGAGAU	1425	11410	UCCACAUCUCCGCUGCUCC	3177
rs362301	11393	GAGCAGCGGAGAU	1426	11393	GAGCAGCGGAGAU	1426	11411	GUCCACAUCUCCGCUGCUC	3178
rs362301	11394	AGCAGCGGAGAU	1427	11394	AGCAGCGGAGAU	1427	11412	AGUCCACAUCUCCGCUGCU	3179
rs362301	11395	GCAGCGGAGAU	1428	11395	GCAGCGGAGAU	1428	11413	AAGUCCACAUCUCCGCUGC	3180
rs362301	11396	CAGCGGAGAU	1429	11396	CAGCGGAGAU	1429	11414	CAAGUCCACAUCUCCGCUG	3181
rs362301	11397	AGCGGAGAU	1430	11397	AGCGGAGAU	1430	11415	ACAAGUCCACAUCUCCGCUG	3182
rs362301	11398	GCGGAGAU	1431	11398	GCGGAGAU	1431	11416	UACAAGUCCACAUCUCCGC	3183
rs362301	11399	CGGAGAU	1432	11399	CGGAGAU	1432	11417	AUACAAGUCCACAUCUCCG	3184
rs362301	11400	GGAGAU	1433	11400	GGAGAU	1433	11418	CAUACAAGUCCACAUCUCC	3185
rs6148278	11440	AGCUGAAAGGAGCCCCUG	1434	11440	AGCUGAAAGGAGCCCCUG	1434	11458	CAGGGGCUCCUUUCAGCU	3186
rs6148278	11441	GCUGAAAGGAGCCCCUGC	1435	11441	GCUGAAAGGAGCCCCUGC	1435	11459	GCAGGGCUCCUUUCAGC	3187
rs6148278	11442	CUGAAAGGAGCCCCUGCU	1436	11442	CUGAAAGGAGCCCCUGCU	1436	11460	AGCAGGGGCUCCUUUCAG	3188
rs6148278	11443	UGAAAGGAGCCCCUGCUC	1437	11443	UGAAAGGAGCCCCUGCUC	1437	11461	GAGCAGGGGCUCCUUUCA	3189
rs6148278	11444	GAAAGGAGCCCCUGCUCA	1438	11444	GAAAGGAGCCCCUGCUCA	1438	11462	UGAGCAGGGGCUCCUUUC	3190
rs6148278	11445	AAAGGGAGCCCCUGCUCAA	1439	11445	AAAGGGAGCCCCUGCUCAA	1439	11463	UUGAGCAGGGGCUCCUUU	3191

rs6148278	11446	AAGGAGCCCCUGCUCAAA	1440	11446	AAGGAGCCCCUGCUCAAA	1440	11464	UUUGAGCAGGGGCUCCCUU	3192
rs6148278	11447	AGGAGCCCCUGCUCAAAG	1441	11447	AGGAGCCCCUGCUCAAAG	1441	11465	CUUUGAGCAGGGGCUCCCU	3193
rs6148278	11448	GGAGCCCCUGCUCAAAGG	1442	11448	GGAGCCCCUGCUCAAAGG	1442	11466	CCUUUGAGCAGGGGCUCC	3194
rs6148278	11449	GGAGCCCCUGCUCAAAGGG	1443	11449	GGAGCCCCUGCUCAAAGGG	1443	11467	CCCUUUGAGCAGGGGCUCC	3195
rs6148278	11450	GAGCCCCUGCUCAAAGGGA	1444	11450	GAGCCCCUGCUCAAAGGGA	1444	11468	UCCCUUUGAGCAGGGGCU	3196
rs6148278	11451	AGCCCCUGCUCAAAGGGAG	1445	11451	AGCCCCUGCUCAAAGGGAG	1445	11469	CUCCCUUUGAGCAGGGGCU	3197
rs6148278	11452	GCCCCUGCUCAAAGGGAGC	1446	11452	GCCCCUGCUCAAAGGGAGC	1446	11470	GCUCCCUUUGAGCAGGGGC	3198
rs6148278	11453	CCCCUGCUCAAAGGGAGCC	1447	11453	CCCCUGCUCAAAGGGAGCC	1447	11471	GGCUCCCUUUGAGCAGGGG	3199
rs6148278	11454	CCUGCUCAAAGGGAGCCC	1448	11454	CCUGCUCAAAGGGAGCCC	1448	11472	GGGUCCCUUUGAGCAGGG	3200
rs6148278	11455	CCUGCUCAAAGGGAGCCCC	1449	11455	CCUGCUCAAAGGGAGCCCC	1449	11473	GGGGUCCCUUUGAGCAGG	3201
rs6148278	11456	CUGCUCAAAGGGAGCCCCU	1450	11456	CUGCUCAAAGGGAGCCCCU	1450	11474	AGGGUCCCUUUGAGCAGC	3202
rs6148278	11457	UGCUCAAAGGGAGCCCCUC	1451	11457	UGCUCAAAGGGAGCCCCUC	1451	11475	GAGGGUCCCUUUGAGCA	3203
rs6148278	11458	GCUCAAAGGGAGCCCCUCC	1452	11458	GCUCAAAGGGAGCCCCUCC	1452	11476	GGAGGGUCCCUUUGAGC	3204
rs6148278	11459	CUCAAAGGGAGCCCCUCU	1453	11459	CUCAAAGGGAGCCCCUCU	1453	11477	AGGAGGGUCCCUUUGAG	3205
rs6148278	11460	UCAAGGGAGCCCCUCCUC	1454	11460	UCAAGGGAGCCCCUCCUC	1454	11478	GAGGAGGGUCCCUUUGA	3206
rs6148278	11461	CAAAGGGAGCCCCUCCUCU	1455	11461	CAAAGGGAGCCCCUCCUCU	1455	11479	AGAGGAGGGUCCCUUUG	3207
rs6148278	11440	AGCUGAAAGGGAGCCCCUC	1456	11440	AGCUGAAAGGGAGCCCCUC	1456	11458	GAGGGUCCCUUUGAGCU	3208
rs6148278	11441	GCUGAAAGGGAGCCCCUCC	1457	11441	GCUGAAAGGGAGCCCCUCC	1457	11459	GGAGGGUCCCUUUGAGC	3209
rs6148278	11442	CUGAAAGGGAGCCCCUCCU	1458	11442	CUGAAAGGGAGCCCCUCCU	1458	11460	AGAGGGUCCCUUUGAG	3210
rs6148278	11443	UGAAAGGGAGCCCCUCCUC	1459	11443	UGAAAGGGAGCCCCUCCUC	1459	11461	GAGAGGGUCCCUUUGA	3211
rs6148278	11444	GAAAGGGAGCCCCUCCUCU	1460	11444	GAAAGGGAGCCCCUCCUCU	1460	11462	AGAGAGGGUCCCUUUC	3212
rs5855773	11641	GUAGAAAAUCACCAUUCU	1461	11641	GUAGAAAAUCACCAUUCU	1461	11659	AGAAUGGUGAUUUUCUAC	3213
rs5855773	11642	UAAGAAAAUCACCAUUCUU	1462	11642	UAAGAAAAUCACCAUUCUU	1462	11660	AAGAAUGGUGAUUUUCUA	3214
rs5855773	11643	AAGAAAAUCACCAUUCUUC	1463	11643	AAGAAAAUCACCAUUCUUC	1463	11661	GAAGAAUGGUGAUUUUCU	3215
rs5855773	11644	AGAAAAUCACCAUUCUUC	1464	11644	AGAAAAUCACCAUUCUUC	1464	11662	GGAAGAAUGGUGAUUUUCU	3216
rs5855773	11645	GAAAAUCACCAUUCUUC	1465	11645	GAAAAUCACCAUUCUUC	1465	11663	CGGAAGAAUGGUGAUUUUC	3217
rs5855773	11646	AAAAUCACCAUUCUUC	1466	11646	AAAAUCACCAUUCUUC	1466	11664	ACGGAAGAAUGGUGAUUUU	3218
rs5855773	11647	AAUACACCAUUCUUC	1467	11647	AAUACACCAUUCUUC	1467	11665	UACGGAAGAAUGGUGAUUU	3219
rs5855773	11648	AUACACCAUUCUUC	1468	11648	AUACACCAUUCUUC	1468	11666	AUACGGAAGAAUGGUGAUU	3220
rs5855773	11649	AUCACCAUUCUUC	1469	11649	AUCACCAUUCUUC	1469	11667	AUACGGAAGAAUGGUGAU	3221
rs5855773	11650	UCACCAUUCUUC	1470	11650	UCACCAUUCUUC	1470	11668	CAUACGGAAGAAUGGUGA	3222
rs5855773	11651	CACCAUUCUUC	1471	11651	CACCAUUCUUC	1471	11669	CCAAUACGGAAGAAUGGUG	3223
rs5855773	11652	ACCAUUCUUC	1472	11652	ACCAUUCUUC	1472	11670	ACCAAUACGGAAGAAUGGU	3224
rs5855773	11653	CCAUUCUUC	1473	11653	CCAUUCUUC	1473	11671	AACCAAUACGGAAGAAUGG	3225
rs5855773	11654	CAUUCUUC	1474	11654	CAUUCUUC	1474	11672	CAACCAAUACGGAAGAAUG	3226
rs5855773	11655	AUUCUUC	1475	11655	AUUCUUC	1475	11673	CCAAACCAAUACGGAAGAAU	3227
rs5855773	11656	UUCUUC	1476	11656	UUCUUC	1476	11674	CCCAACCAAUACGGAAGAA	3228
rs5855773	11641	GUAGAAAAUCACCAUUC	1477	11641	GUAGAAAAUCACCAUUC	1477	11659	GGAAUGGUGAUUUUCUAC	3229
rs5855773	11642	UAAGAAAAUCACCAUUC	1478	11642	UAAGAAAAUCACCAUUC	1478	11660	CGGAUGGUGAUUUUCUUA	3230

rs5855773	11643	AAGAAAUCACCAUUCGUA	1479	11643	AAGAAAUCACCAUUCGUA	1479	11661	ACGGAAUGGUGAUUUUCUU	3231
rs5855773	11644	AGAAAUCACCAUUCGUA	1480	11644	AGAAAUCACCAUUCGUA	1480	11662	UACGGAAUGGUGAUUUUCU	3232
rs5855773	11645	GAAAUCACCAUUCGUAU	1481	11645	GAAAUCACCAUUCGUAU	1481	11663	AUACGGAAUGGUGAUUUUC	3233
rs5855773	11646	AAAAUCACCAUUCGUAUU	1482	11646	AAAAUCACCAUUCGUAUU	1482	11664	AUACGGAAUGGUGAUUUU	3234
rs5855773	11647	AAAUACACCAUUCGUAUUG	1483	11647	AAAUACACCAUUCGUAUUG	1483	11665	CAAUACGGAAUGGUGAUUU	3235
rs5855773	11648	AUACACCAUUCGUAUUGG	1484	11648	AUACACCAUUCGUAUUGG	1484	11666	CCAAUACGGAAUGGUGAUU	3236
rs5855773	11649	AUACCAUUCGUAUUGGU	1485	11649	AUACCAUUCGUAUUGGU	1485	11667	ACCAAUACGGAAUGGUGAU	3237
rs5855773	11650	UCACCAUUCGUAUUGGUU	1486	11650	UCACCAUUCGUAUUGGUU	1486	11668	AACCAAUACGGAAUGGUGA	3238
rs5855773	11651	CACCAUUCGUAUUGGUUG	1487	11651	CACCAUUCGUAUUGGUUG	1487	11669	CAACCAAUACGGAAUGGUG	3239
rs5855773	11652	ACCAUUCGUAUUGGUUGG	1488	11652	ACCAUUCGUAUUGGUUGG	1488	11670	CCAAACCAUACGGAAUGGU	3240
rs5855773	11653	CCAUUCGUAUUGGUUGGG	1489	11653	CCAUUCGUAUUGGUUGGG	1489	11671	CCAAACCAUACGGAAUGGG	3241
rs5855774	11740	AGUUCUCAGAACUGUUGC	1490	11740	AGUUCUCAGAACUGUUGC	1490	11758	GCAACAGUUCUGAGAACUU	3242
rs5855774	11741	AGUUCUCAGAACUGUUGCU	1491	11741	AGUUCUCAGAACUGUUGCU	1491	11759	AGCAACAGUUCUGAGAACU	3243
rs5855774	11742	GUUCUCAGAACUGUUGCUG	1492	11742	GUUCUCAGAACUGUUGCUG	1492	11760	CAGCAACAGUUCUGAGAAC	3244
rs5855774	11743	UUCUCAGAACUGUUGCUGC	1493	11743	UUCUCAGAACUGUUGCUGC	1493	11761	GCAGCAACAGUUCUGAGAA	3245
rs5855774	11744	UCUCAGAACUGUUGCUGCU	1494	11744	UCUCAGAACUGUUGCUGCU	1494	11762	AGCAGCAACAGUUCUGAGA	3246
rs5855774	11745	CUCAGAACUGUUGCUGCUC	1495	11745	CUCAGAACUGUUGCUGCUC	1495	11763	GAGCAGCAACAGUUCUGAG	3247
rs5855774	11746	UCAGAACUGUUGCUGCUC	1496	11746	UCAGAACUGUUGCUGCUC	1496	11764	GGAGCAGCAACAGUUCUGA	3248
rs5855774	11747	CAGAACUGUUGCUGCUC	1497	11747	CAGAACUGUUGCUGCUC	1497	11765	GGGAGCAGCAACAGUUCUG	3249
rs5855774	11748	AGAACUGUUGCUGCUC	1498	11748	AGAACUGUUGCUGCUC	1498	11766	GGGAGCAGCAACAGUUCU	3250
rs5855774	11749	GAACUGUUGCUGCUC	1499	11749	GAACUGUUGCUGCUC	1499	11767	UGGGAGCAGCAACAGUUC	3251
rs5855774	11750	AACUGUUGCUGCUC	1500	11750	AACUGUUGCUGCUC	1500	11768	GUGGGAGCAGCAACAGU	3252
rs5855774	11751	ACUGUUGCUGCUC	1501	11751	ACUGUUGCUGCUC	1501	11769	GGUGGGAGCAGCAACAGU	3253
rs5855774	11752	CUGUUGCUGCUC	1502	11752	CUGUUGCUGCUC	1502	11770	GGUGGGAGCAGCAACAG	3254
rs5855774	11753	UGUUGCUGCUC	1503	11753	UGUUGCUGCUC	1503	11771	CGGUGGGAGCAGCAACA	3255
rs5855774	11754	GUUGCUGCUC	1504	11754	GUUGCUGCUC	1504	11772	GCGGUGGGAGCAGCAAC	3256
rs5855774	11755	UUGCUGCUC	1505	11755	UUGCUGCUC	1505	11773	GGCGGUGGGAGCAGCAA	3257
rs5855774	11756	UGCUGCUC	1506	11756	UGCUGCUC	1506	11774	AGCGGUGGGAGCAGCA	3258
rs5855774	11740	AAGUUCUCAGAACUGUUGG	1507	11740	AAGUUCUCAGAACUGUUGG	1507	11758	CCAACAGUUCUGAGAACUU	3259
rs5855774	11741	AGUUCUCAGAACUGUUGGC	1508	11741	AGUUCUCAGAACUGUUGGC	1508	11759	GCCAACAGUUCUGAGAACU	3260
rs5855774	11742	GUUCUCAGAACUGUUGGCU	1509	11742	GUUCUCAGAACUGUUGGCU	1509	11760	AGCCAACAGUUCUGAGAAC	3261
rs5855774	11743	UUCUCAGAACUGUUGGCUG	1510	11743	UUCUCAGAACUGUUGGCUG	1510	11761	CAGCCAACAGUUCUGAGAA	3262
rs5855774	11744	UCUCAGAACUGUUGGCUGC	1511	11744	UCUCAGAACUGUUGGCUGC	1511	11762	GCAGCCAACAGUUCUGAGA	3263
rs5855774	11745	CUCAGAACUGUUGGCUGCU	1512	11745	CUCAGAACUGUUGGCUGCU	1512	11763	AGCAGCCAACAGUUCUGAG	3264
rs5855774	11746	UCAGAACUGUUGGCUGCUC	1513	11746	UCAGAACUGUUGGCUGCUC	1513	11764	GAGCAGCCAACAGUUCUGA	3265
rs5855774	11747	CAGAACUGUUGGCUGCUC	1514	11747	CAGAACUGUUGGCUGCUC	1514	11765	GGAGCAGCCAACAGUUCUG	3266
rs5855774	11748	AGAACUGUUGGCUGCUC	1515	11748	AGAACUGUUGGCUGCUC	1515	11766	GGGAGCAGCCAACAGUUCU	3267
rs5855774	11749	GAACUGUUGGCUGCUC	1516	11749	GAACUGUUGGCUGCUC	1516	11767	GGGAGCAGCCAACAGUUC	3268
rs5855774	11750	AACUGUUGGCUGCUC	1517	11750	AACUGUUGGCUGCUC	1517	11768	UGGGAGCAGCCAACAGUU	3269

rs5855774	11751	ACUGUUGGCGUCUCCCCAC	1518	11751	ACUGUUGGCGUCUCCCCAC	1518	11769	GUGGGGAGCAGCCAAACAGU	3270
rs5855774	11752	CUGUUGGCGUCUCCCCACC	1519	11752	CUGUUGGCGUCUCCCCACC	1519	11770	GUGGGGAGCAGCCAAACAG	3271
rs5855774	11753	UGUUGGCGUCUCCCCACC	1520	11753	UGUUGGCGUCUCCCCACC	1520	11771	GUGGGGAGCAGCCAAACA	3272
rs5855774	11754	GUUGGCGUCUCCCCACCG	1521	11754	GUUGGCGUCUCCCCACCG	1521	11772	CGGGUGGGAGCAGCCAAAC	3273
rs5855774	11755	UUGGCGUCUCCCCACCGC	1522	11755	UUGGCGUCUCCCCACCGC	1522	11773	GCGGUGGGGAGCAGCCAA	3274
rs5855774	11756	UGGCGUCUCCCCACCGCC	1523	11756	UGGCGUCUCCCCACCGCC	1523	11774	GGCGGUGGGGAGCAGCCA	3275
rs5855774	11757	GGCGUCUCCCCACCGCCU	1524	11757	GGCGUCUCCCCACCGCCU	1524	11775	AGCGGGUGGGGAGCAGCC	3276
rs2159172	11846	AGAUGUUUACAUUUGUAAG	1525	11846	AGAUGUUUACAUUUGUAAG	1525	11864	CUUACAAAUGUAAACAUCU	3277
rs2159172	11847	GAUGUUUACAUUUGUAAGA	1526	11847	GAUGUUUACAUUUGUAAGA	1526	11865	UCUUACAAAUGUAAACAUC	3278
rs2159172	11848	AUGUUUACAUUUGUAAGAA	1527	11848	AUGUUUACAUUUGUAAGAA	1527	11866	UUUUACAAAUGUAAACAUC	3279
rs2159172	11849	UGUUUACAUUUGUAAGAAA	1528	11849	UGUUUACAUUUGUAAGAAA	1528	11867	UUUUUACAAAUGUAAACA	3280
rs2159172	11850	GUUUACAUUUGUAAGAAAU	1529	11850	GUUUACAUUUGUAAGAAAU	1529	11868	AUUUUUACAAAUGUAAAC	3281
rs2159172	11851	UUUACAUUUGUAAGAAUA	1530	11851	UUUACAUUUGUAAGAAUA	1530	11869	UAUUUUUACAAAUGUAAA	3282
rs2159172	11852	UUACAUUUGUAAGAAUAA	1531	11852	UUACAUUUGUAAGAAUAA	1531	11870	UUUUUUUACAAAUGUAAA	3283
rs2159172	11853	UACAUUUGUAAGAAUAAC	1532	11853	UACAUUUGUAAGAAUAAC	1532	11871	GUUUUUUUUACAAAUGUA	3284
rs2159172	11854	ACAUUUGUAAGAAUAACA	1533	11854	ACAUUUGUAAGAAUAACA	1533	11872	UGUUUUUUUACAAAUGU	3285
rs2159172	11855	CAUUUGUAAGAAUAACAC	1534	11855	CAUUUGUAAGAAUAACAC	1534	11873	GUGUUUUUUUACAAAUG	3286
rs2159172	11856	AUUUGUAAGAAUAACACU	1535	11856	AUUUGUAAGAAUAACACU	1535	11874	AGUGUUUUUUUACAAAU	3287
rs2159172	11857	UUUGUAAGAAUAACACUG	1536	11857	UUUGUAAGAAUAACACUG	1536	11875	CAGUGUUUUUUUACAAA	3288
rs2159172	11858	UUGUAAGAAUAACACUGU	1537	11858	UUGUAAGAAUAACACUGU	1537	11876	ACAGUUUUUUUACAAAC	3289
rs2159172	11859	UGUAAGAAUAACACUGUG	1538	11859	UGUAAGAAUAACACUGUG	1538	11877	CACAGUUUUUUUACUACA	3290
rs2159172	11860	GUAAGAAUAACACUGUGA	1539	11860	GUAAGAAUAACACUGUGA	1539	11878	UCACAGUUUUUUUACUAC	3291
rs2159172	11861	UAAGAAUAACACUGUGAA	1540	11861	UAAGAAUAACACUGUGAA	1540	11879	UUCACAGUUUUUUUACUUA	3292
rs2159172	11862	AAGAAUAACACUGUGAAU	1541	11862	AAGAAUAACACUGUGAAU	1541	11880	AUUCACAGUUUUUUUACUU	3293
rs2159172	11863	AGAAUAACACUGUGAAUG	1542	11863	AGAAUAACACUGUGAAUG	1542	11881	CAUUCACAGUUUUUUUACU	3294
rs2159172	11864	GAAUAACACUGUGAAUGU	1543	11864	GAAUAACACUGUGAAUGU	1543	11882	ACAUUCACAGUUUUUUUAC	3295
rs2159172	11846	AGAUGUUUACAUUUGUAAA	1544	11846	AGAUGUUUACAUUUGUAAA	1544	11864	UUUACAAAUGUAAACAUC	3296
rs2159172	11847	GAUGUUUACAUUUGUAAAA	1545	11847	GAUGUUUACAUUUGUAAAA	1545	11865	UUUUACAAAUGUAAACAUC	3297
rs2159172	11848	AUGUUUACAUUUGUAAAA	1546	11848	AUGUUUACAUUUGUAAAA	1546	11866	UUUUUACAAAUGUAAACA	3298
rs2159172	11849	UGUUUACAUUUGUAAAAA	1547	11849	UGUUUACAUUUGUAAAAA	1547	11867	UUUUUACAAAUGUAAACA	3299
rs2159172	11850	GUUUACAUUUGUAAAAAU	1548	11850	GUUUACAUUUGUAAAAAU	1548	11868	AUUUUUACAAAUGUAAAC	3300
rs2159172	11851	UUUACAUUUGUAAAAAUA	1549	11851	UUUACAUUUGUAAAAAUA	1549	11869	UAUUUUUACAAAUGUAAA	3301
rs2159172	11852	UUACAUUUGUAAAAAUAA	1550	11852	UUACAUUUGUAAAAAUAA	1550	11870	UUUUUUUUUACAAAUGUA	3302
rs2159172	11853	UACAUUUGUAAAAAUAAC	1551	11853	UACAUUUGUAAAAAUAAC	1551	11871	GUUUUUUUUUUACAAAUGU	3303
rs2159172	11854	ACAUUUGUAAAAAUACA	1552	11854	ACAUUUGUAAAAAUACA	1552	11872	UGUUUUUUUUUACAAAUGU	3304
rs2159172	11855	CAUUUGUAAAAAUACAC	1553	11855	CAUUUGUAAAAAUACAC	1553	11873	GUGUUUUUUUUUACAAAU	3305
rs2159172	11856	AUUUGUAAAAAUACACU	1554	11856	AUUUGUAAAAAUACACU	1554	11874	AGUGUUUUUUUUUACAAAU	3306
rs2159172	11857	UUUGUAAAAAUACACUG	1555	11857	UUUGUAAAAAUACACUG	1555	11875	CAGUGUUUUUUUUUACAAA	3307
rs2159172	11858	UUGUAAAAAUACACUGU	1556	11858	UUGUAAAAAUACACUGU	1556	11876	ACAGUGUUUUUUUUUACAA	3308

rs2159172	11859	UGUAAAAAUAAACACUGUG	1557	11859	UGUAAAAAUAAACACUGUG	1557	11877	CACAGUGUUAUUUUUACA	3309
rs2159172	11860	GUAAAAAUAAACACUGUGA	1558	11860	GUAAAAAUAAACACUGUGA	1558	11878	UCACAGUGUUAUUUUUAC	3310
rs2159172	11861	UAAAAAUAAACACUGUGAA	1559	11861	UAAAAAUAAACACUGUGAA	1559	11879	UUACACAGUGUUAUUUUUA	3311
rs2159172	11862	AAAAAUAAACACUGUGAAU	1560	11862	AAAAAUAAACACUGUGAAU	1560	11880	AUUCACAGUGUUAUUUUUU	3312
rs2159172	11863	AAAAAUAAACACUGUGAAUG	1561	11863	AAAAAUAAACACUGUGAAUG	1561	11881	CAUUCACAGUGUUAUUUUU	3313
rs2159172	11864	AAAAAUAAACACUGUGAAUGU	1562	11864	AAAAAUAAACACUGUGAAUGU	1562	11882	ACAUUCACAGUGUUAUUUU	3314
rs2237008	12640	ACCCUCAUUUCUGCCAGCG	1563	12640	ACCCUCAUUUCUGCCAGCG	1563	12658	CGCUGGCAGAAUAGAGGU	3315
rs2237008	12641	CCUCAUUUCUGCCAGCGC	1564	12641	CCUCAUUUCUGCCAGCGC	1564	12659	GCGCUGGCAGAAUAGAGG	3316
rs2237008	12642	CCUCAUUUCUGCCAGCGCA	1565	12642	CCUCAUUUCUGCCAGCGCA	1565	12660	UGCGCUGGCAGAAUAGAG	3317
rs2237008	12643	CUCAUUUCUGCCAGCGCAU	1566	12643	CUCAUUUCUGCCAGCGCAU	1566	12661	AUGCGCUGGCAGAAUAGAG	3318
rs2237008	12644	UCAUUUCUGCCAGCGCAUG	1567	12644	UCAUUUCUGCCAGCGCAUG	1567	12662	CAUGCGCUGGCAGAAUAG	3319
rs2237008	12645	CAUUCUGCCAGCGCAUGU	1568	12645	CAUUCUGCCAGCGCAUGU	1568	12663	ACAUGCGCUGGCAGAAUAG	3320
rs2237008	12646	AUUCUGCCAGCGCAUGUG	1569	12646	AUUCUGCCAGCGCAUGUG	1569	12664	CACAUGCGCUGGCAGAAU	3321
rs2237008	12647	UUUCUGCCAGCGCAUGUGU	1570	12647	UUUCUGCCAGCGCAUGUGU	1570	12665	ACACAUGCGCUGGCAGAAA	3322
rs2237008	12648	UUCUGCCAGCGCAUGUGUC	1571	12648	UUCUGCCAGCGCAUGUGUC	1571	12666	GACACAUGCGCUGGCAGAA	3323
rs2237008	12649	UCUGCCAGCGCAUGUGUCC	1572	12649	UCUGCCAGCGCAUGUGUCC	1572	12667	GGACACAUGCGCUGGCAG	3324
rs2237008	12650	CUGCCAGCGCAUGUGUCCU	1573	12650	CUGCCAGCGCAUGUGUCCU	1573	12668	AGGACACAUGCGCUGGCAG	3325
rs2237008	12651	UGCCAGCGCAUGUGUCCUU	1574	12651	UGCCAGCGCAUGUGUCCUU	1574	12669	AAGGACACAUGCGCUGGCA	3326
rs2237008	12652	GCCAGCGCAUGUGUCCUUU	1575	12652	GCCAGCGCAUGUGUCCUUU	1575	12670	AAAGGACACAUGCGCUGGC	3327
rs2237008	12653	CCAGCGCAUGUGUCCUUUC	1576	12653	CCAGCGCAUGUGUCCUUUC	1576	12671	GAAAGGACACAUGCGCUGG	3328
rs2237008	12654	CAGCGCAUGUGUCCUUUCA	1577	12654	CAGCGCAUGUGUCCUUUCA	1577	12672	UGAAAGGACACAUGCGCUG	3329
rs2237008	12655	AGCGCAUGUGUCCUUUCA	1578	12655	AGCGCAUGUGUCCUUUCA	1578	12673	UUGAAAGGACACAUGCGCU	3330
rs2237008	12656	GCGCAUGUGUCCUUUCAAG	1579	12656	GCGCAUGUGUCCUUUCAAG	1579	12674	CUUGAAAGGACACAUGCGC	3331
rs2237008	12657	CGCAUGUGUCCUUUCAAGG	1580	12657	CGCAUGUGUCCUUUCAAGG	1580	12675	CCUUGAAAGGACACAUGCG	3332
rs2237008	12658	GCAUGUGUCCUUUCAAGGG	1581	12658	GCAUGUGUCCUUUCAAGGG	1581	12676	CCCUUGAAAGGACACAUGC	3333
rs2237008	12640	ACCCUCAUUUCUGCCAGCA	1582	12640	ACCCUCAUUUCUGCCAGCA	1582	12658	UGCUGGCAGAAUAGAGGU	3334
rs2237008	12641	CCUCAUUUCUGCCAGCAC	1583	12641	CCUCAUUUCUGCCAGCAC	1583	12659	GUGCUGGCAGAAUAGAGG	3335
rs2237008	12642	CCUCAUUUCUGCCAGCACA	1584	12642	CCUCAUUUCUGCCAGCACA	1584	12660	UGUGCUGGCAGAAUAGAG	3336
rs2237008	12643	CUCAUUUCUGCCAGCACAU	1585	12643	CUCAUUUCUGCCAGCACAU	1585	12661	AUGUGCUGGCAGAAUAGAG	3337
rs2237008	12644	UCAUUUCUGCCAGCACAU	1586	12644	UCAUUUCUGCCAGCACAU	1586	12662	CAUGUGCUGGCAGAAUAG	3338
rs2237008	12645	CAUUCUGCCAGCACAU	1587	12645	CAUUCUGCCAGCACAU	1587	12663	ACAUGUGCUGGCAGAAUAG	3339
rs2237008	12646	AUUCUGCCAGCACAU	1588	12646	AUUCUGCCAGCACAU	1588	12664	CACAUGUGCUGGCAGAAU	3340
rs2237008	12647	UUUCUGCCAGCACAU	1589	12647	UUUCUGCCAGCACAU	1589	12665	ACACAUGUGCUGGCAGAAA	3341
rs2237008	12648	UUCUGCCAGCACAU	1590	12648	UUCUGCCAGCACAU	1590	12666	GACACAUGUGCUGGCAGAA	3342
rs2237008	12649	UCUGCCAGCACAU	1591	12649	UCUGCCAGCACAU	1591	12667	GGACACAUGUGCUGGCAG	3343
rs2237008	12650	CUGCCAGCACAU	1592	12650	CUGCCAGCACAU	1592	12668	AGGACACAUGUGCUGGCAG	3344
rs2237008	12651	UGCCAGCACAU	1593	12651	UGCCAGCACAU	1593	12669	AAGGACACAUGUGCUGGCA	3345
rs2237008	12652	GCCAGCACAU	1594	12652	GCCAGCACAU	1594	12670	AAAGGACACAUGUGCUGGC	3346
rs2237008	12653	CCAGCACAU	1595	12653	CCAGCACAU	1595	12671	GAAAGGACACAUGUGCUGG	3347

rs2237008	12654	CAGCACAUGUGUCCUUUCA	1596	12654	CAGCACAUGUGUCCUUUCA	1596	12672	UGAAAGGACACAUGUGCUG	3348
rs2237008	12655	AGCACAUGUGUCCUUUCA	1597	12655	AGCACAUGUGUCCUUUCA	1597	12673	UUGAAAGGACACAUGUCU	3349
rs2237008	12656	GCACAUGUGUCCUUUCAAG	1598	12656	GCACAUGUGUCCUUUCAAG	1598	12674	CUUGAAAGGACACAUGGC	3350
rs2237008	12657	CACAUGUGUCCUUUCAAGG	1599	12657	CACAUGUGUCCUUUCAAGG	1599	12675	CCUUGAAAGGACACAUGUG	3351
rs2237008	12658	ACAUGUGUCCUUUCAAGGG	1600	12658	ACAUGUGUCCUUUCAAGGG	1600	12676	CCUUGAAAGGACACAUGU	3352
rs362300	12893	CAGGUGGAACUUCUCCCG	1601	12893	CAGGUGGAACUUCUCCCG	1601	12911	CGGGAGGAAGUUCACCUG	3353
rs362300	12894	AGGUGGAACUUCUCCCGU	1602	12894	AGGUGGAACUUCUCCCGU	1602	12912	ACGGAGGAAGUUCACCUCU	3354
rs362300	12895	GGUGGAACUUCUCCCGUUG	1603	12895	GGUGGAACUUCUCCCGUUG	1603	12913	AACGGAGGAAGUUCACC	3355
rs362300	12896	GUGGAACUUCUCCCGUUG	1604	12896	GUGGAACUUCUCCCGUUG	1604	12914	CAACGGAGGAAGUUCAC	3356
rs362300	12897	UGGAACUUCUCCCGUUGC	1605	12897	UGGAACUUCUCCCGUUGC	1605	12915	GCAACGGAGGAAGUCCA	3357
rs362300	12898	GGAACUUCUCCCGUUGCG	1606	12898	GGAACUUCUCCCGUUGCG	1606	12916	CGCAACGGAGGAAGUCC	3358
rs362300	12899	GAACUUCUCCCGUUGCGG	1607	12899	GAACUUCUCCCGUUGCGG	1607	12917	CCGCAACGGAGGAAGUUC	3359
rs362300	12900	AACUUCUCCCGUUGCGGG	1608	12900	AACUUCUCCCGUUGCGGG	1608	12918	CCCGCAACGGAGGAAGU	3360
rs362300	12901	ACUUCUCCCGUUGCGGGG	1609	12901	ACUUCUCCCGUUGCGGGG	1609	12919	CCCCGCAACGGAGGAAGU	3361
rs362300	12902	CUUCUCCCGUUGCGGGGU	1610	12902	CUUCUCCCGUUGCGGGGU	1610	12920	ACCCGCAACGGAGGAAG	3362
rs362300	12903	UUCUCCCGUUGCGGGGUG	1611	12903	UUCUCCCGUUGCGGGGUG	1611	12921	CACCCGCAACGGAGGA	3363
rs362300	12904	UCCUCCCGUUGCGGGUGG	1612	12904	UCCUCCCGUUGCGGGUGG	1612	12922	CCACCCGCAACGGAGGA	3364
rs362300	12905	CUCCCGUUGCGGGUGGA	1613	12905	CUCCCGUUGCGGGUGGA	1613	12923	UCCACCCGCAACGGAGG	3365
rs362300	12906	CUCCCGUUGCGGGUGGAG	1614	12906	CUCCCGUUGCGGGUGGAG	1614	12924	CUCCACCCGCAACGGGAG	3366
rs362300	12907	UCCCGUUGCGGGUGGAGU	1615	12907	UCCCGUUGCGGGUGGAGU	1615	12925	ACUCCACCCGCAACGGGA	3367
rs362300	12908	CCCGUUGCGGGUGGAGUG	1616	12908	CCCGUUGCGGGUGGAGUG	1616	12926	CACUCCACCCGCAACGGG	3368
rs362300	12909	CCGUUGCGGGUGGAGUGA	1617	12909	CCGUUGCGGGUGGAGUGA	1617	12927	UCACUCCACCCGCAACGG	3369
rs362300	12910	CGUUGCGGGUGGAGUGAG	1618	12910	CGUUGCGGGUGGAGUGAG	1618	12928	CUCACUCCACCCGCAACG	3370
rs362300	12911	GUUGCGGGUGGAGUGAGG	1619	12911	GUUGCGGGUGGAGUGAGG	1619	12929	CCUCACUCCACCCGCAAC	3371
rs362300	12893	CAGGUGGAACUUCUCCCA	1620	12893	CAGGUGGAACUUCUCCCA	1620	12911	UGGGAGGAAGUUCACCUG	3372
rs362300	12894	AGGUGGAACUUCUCCCAU	1621	12894	AGGUGGAACUUCUCCCAU	1621	12912	AUGGGAGGAAGUUCACCUCU	3373
rs362300	12895	GGUGGAACUUCUCCCAUUG	1622	12895	GGUGGAACUUCUCCCAUUG	1622	12913	AUUGGGAGGAAGUUCACC	3374
rs362300	12896	GUGGAACUUCUCCCAUUG	1623	12896	GUGGAACUUCUCCCAUUG	1623	12914	CAAUGGGAGGAAGUUCACC	3375
rs362300	12897	UGGAACUUCUCCCAUUGC	1624	12897	UGGAACUUCUCCCAUUGC	1624	12915	GCAUUGGGAGGAAGUCCA	3376
rs362300	12898	GGAACUUCUCCCAUUGCG	1625	12898	GGAACUUCUCCCAUUGCG	1625	12916	CGCAUUGGGAGGAAGUCC	3377
rs362300	12899	GAACUUCUCCCAUUGCGG	1626	12899	GAACUUCUCCCAUUGCGG	1626	12917	CCGCAUUGGGAGGAAGUUC	3378
rs362300	12900	AACUUCUCCCAUUGCGGG	1627	12900	AACUUCUCCCAUUGCGGG	1627	12918	CCCGCAUUGGGAGGAAGU	3379
rs362300	12901	ACUUCUCCCAUUGCGGGG	1628	12901	ACUUCUCCCAUUGCGGGG	1628	12919	CCCCGCAUUGGGAGGAAGU	3380
rs362300	12902	CUUCUCCCAUUGCGGGGU	1629	12902	CUUCUCCCAUUGCGGGGU	1629	12920	ACCCGCAUUGGGAGGAAG	3381
rs362300	12903	UUCUCCCAUUGCGGGGUG	1630	12903	UUCUCCCAUUGCGGGGUG	1630	12921	CACCCGCAUUGGGAGGA	3382
rs362300	12904	UCCUCCCAUUGCGGGUGG	1631	12904	UCCUCCCAUUGCGGGUGG	1631	12922	CCACCCGCAUUGGGAGGA	3383
rs362300	12905	CUCCCAUUGCGGGUGGA	1632	12905	CUCCCAUUGCGGGUGGA	1632	12923	UCCACCCGCAUUGGGAGG	3384
rs362300	12906	CUCCCAUUGCGGGUGGAG	1633	12906	CUCCCAUUGCGGGUGGAG	1633	12924	CUCCACCCGCAUUGGGAG	3385
rs362300	12907	UCCCAUUGCGGGUGGAGU	1634	12907	UCCCAUUGCGGGUGGAGU	1634	12925	ACUCCACCCGCAUUGGGA	3386

rs362300	12908	CCAUUGCGGGGUGGAGUG	1635	12908	CCAUUGCGGGGUGGAGUG	1635	12926	CACUCCACCCCGCAAUGGG	3387
rs362300	12909	CCAUUGCGGGGUGGAGUGA	1636	12909	CCAUUGCGGGGUGGAGUGA	1636	12927	UCACUCCACCCCGCAAUGG	3388
rs362300	12910	CAUUGCGGGGUGGAGUGAG	1637	12910	CAUUGCGGGGUGGAGUGAG	1637	12928	CUCACUCCACCCCGCAAUG	3389
rs362300	12911	AUUGCGGGGUGGAGUGAGG	1638	12911	AUUGCGGGGUGGAGUGAGG	1638	12929	CCUACUCCACCCCGCAAU	3390
rs2530595	13022	CCCCGUUCCUCCUCUGC	1639	13022	CCCCGUUCCUCCUCUGC	1639	13040	GCAGAGGGAGGAAGCGGGG	3391
rs2530595	13023	CCCGCUUCCUCCUCUGCG	1640	13023	CCCGCUUCCUCCUCUGCG	1640	13041	CGCAGAGGGAGGAAGCGGG	3392
rs2530595	13024	CCGCUUCCUCCUCUGCGG	1641	13024	CCGCUUCCUCCUCUGCGG	1641	13042	CCGCAGAGGGAGGAAGCGG	3393
rs2530595	13025	CGCUUCCUCCUCUGCGGG	1642	13025	CGCUUCCUCCUCUGCGGG	1642	13043	CCCGCAGAGGGAGGAAGCG	3394
rs2530595	13026	GCUUCUCCUCCUCUGCGGG	1643	13026	GCUUCUCCUCCUCUGCGGG	1643	13044	CCCCGCAGAGGGAGGAAGC	3395
rs2530595	13027	CUUCCUCCUCCUCUGCGGGA	1644	13027	CUUCCUCCUCCUCUGCGGGA	1644	13045	UCCCCGCAGAGGGAGGAAG	3396
rs2530595	13028	UUCUCCUCCUCUGCGGGGAG	1645	13028	UUCUCCUCCUCUGCGGGGAG	1645	13046	UCCCCGCAGAGGGAGGA	3397
rs2530595	13029	UCCUCCUCCUCUGCGGGAGG	1646	13029	UCCUCCUCCUCUGCGGGAGG	1646	13047	CUUCCCCGCAGAGGGAGGA	3398
rs2530595	13030	CCUCCUCCUCUGCGGGAGGA	1647	13030	CCUCCUCCUCUGCGGGAGGA	1647	13048	UCCUCCCCGCAGAGGGAGG	3399
rs2530595	13031	CUCCUCCUCUGCGGGAGGAC	1648	13031	CUCCUCCUCUGCGGGAGGAC	1648	13049	GUCCUCCCCGCAGAGGGAG	3400
rs2530595	13032	UCCUCCUCUGCGGGAGGACC	1649	13032	UCCUCCUCUGCGGGAGGACC	1649	13050	GGUCCUCCCCGCAGAGGGA	3401
rs2530595	13033	CCUCCUCCUCUGCGGGAGACC	1650	13033	CCUCCUCCUCUGCGGGAGACC	1650	13051	GGGUCCUCCCCGCAGAGGG	3402
rs2530595	13034	CCUCUGCGGGAGGACCCG	1651	13034	CCUCUGCGGGAGGACCCG	1651	13052	CGGGUCCUCCCCGCAGAGG	3403
rs2530595	13035	CUCUGCGGGAGGACCCGG	1652	13035	CUCUGCGGGAGGACCCGG	1652	13053	CCGGGUCCUCCCCGCAGAG	3404
rs2530595	13036	UCUGCGGGAGGACCCGGG	1653	13036	UCUGCGGGAGGACCCGGG	1653	13054	CCGGGUCCUCCCCGCAGAG	3405
rs2530595	13037	CUGCGGGAGGACCCGGGA	1654	13037	CUGCGGGAGGACCCGGGA	1654	13055	UCCCGGUCCUCCCCGCAG	3406
rs2530595	13038	UGCGGGAGGACCCGGGAC	1655	13038	UGCGGGAGGACCCGGGAC	1655	13056	GUCCCGGUCCUCCCCGCAG	3407
rs2530595	13039	GCGGGAGGACCCGGGACC	1656	13039	GCGGGAGGACCCGGGACC	1656	13057	GGUCCCGGUCCUCCCCGC	3408
rs2530595	13040	CGGGAGGACCCGGGACCA	1657	13040	CGGGAGGACCCGGGACCA	1657	13058	UGGUCCCGGUCCUCCCCGC	3409
rs2530595	13022	CCCCGUUCCUCCUCUGU	1658	13022	CCCCGUUCCUCCUCUGU	1658	13040	ACAGAGGGAGGAAGCGGGG	3410
rs2530595	13023	CCCGCUUCCUCCUCUGUG	1659	13023	CCCGCUUCCUCCUCUGUG	1659	13041	CACAGAGGGAGGAAGCGGG	3411
rs2530595	13024	CCGCUUCCUCCUCUGUGG	1660	13024	CCGCUUCCUCCUCUGUGG	1660	13042	CCACAGAGGGAGGAAGCGG	3412
rs2530595	13025	CGCUUCCUCCUCUGUGGG	1661	13025	CGCUUCCUCCUCUGUGGG	1661	13043	CCCACAGAGGGAGGAAGC	3413
rs2530595	13026	GCUUCUCCUCCUCUGUGGG	1662	13026	GCUUCUCCUCCUCUGUGGG	1662	13044	CCCCACAGAGGGAGGAAGC	3414
rs2530595	13027	CUUCCUCCUCCUCUGUGGGA	1663	13027	CUUCCUCCUCCUCUGUGGGA	1663	13045	UCCCCACAGAGGGAGGAAG	3415
rs2530595	13028	UUCUCCUCCUCUGUGGGAG	1664	13028	UUCUCCUCCUCUGUGGGAG	1664	13046	UCCCCACAGAGGGAGGA	3416
rs2530595	13029	UCCUCCUCCUCUGUGGGAGG	1665	13029	UCCUCCUCCUCUGUGGGAGG	1665	13047	CCUCCCCACAGAGGGAGGA	3417
rs2530595	13030	CCUCCUCCUCUGUGGGAGGA	1666	13030	CCUCCUCCUCUGUGGGAGGA	1666	13048	UCCUCCCCACAGAGGGAGG	3418
rs2530595	13031	CUCCUCCUCUGUGGGAGGAC	1667	13031	CUCCUCCUCUGUGGGAGGAC	1667	13049	GUCCUCCCCACAGAGGGAG	3419
rs2530595	13032	UCCUCCUCUGUGGGAGGACC	1668	13032	UCCUCCUCUGUGGGAGGACC	1668	13050	GGUCCUCCCCACAGAGGGA	3420
rs2530595	13033	CCUCCUCCUCUGGGAGGACCC	1669	13033	CCUCCUCCUCUGGGAGGACCC	1669	13051	GGGUCCUCCCCACAGAGGG	3421
rs2530595	13034	CCUCUGUGGGAGGACCCCG	1670	13034	CCUCUGUGGGAGGACCCCG	1670	13052	CGGUCCUCCCCACAGAGG	3422
rs2530595	13035	CUCUGUGGGAGGACCCCGG	1671	13035	CUCUGUGGGAGGACCCCGG	1671	13053	CCGGUCCUCCCCACAGAG	3423
rs2530595	13036	UCUGUGGGAGGACCCCGGG	1672	13036	UCUGUGGGAGGACCCCGGG	1672	13054	CCCGGUCCUCCCCACAGAG	3424
rs2530595	13037	CUGUGGGAGGACCCCGGGA	1673	13037	CUGUGGGAGGACCCCGGGA	1673	13055	UCCCGGUCCUCCCCACAG	3425

rs2530595	13038	UGUGGGGAGGACCCGGGAC	1674	13038	UGUGGGGAGGACCCGGGAC	1674	13056	GUCCCCGGGUCCUCCCCACA	3426
rs2530595	13039	GUGGGGAGGACCCGGGACC	1675	13039	GUGGGGAGGACCCGGGACC	1675	13057	GGUCCCCGGGUCCUCCCCAC	3427
rs2530595	13040	UGGGGAGGACCCGGGACCA	1676	13040	UGGGGAGGACCCGGGACCA	1676	13058	UGGUCCCCGGGUCCUCCCCA	3428
rs1803770	13464	CUGCUUUGCACCCGUGGUCA	1677	13464	CUGCUUUGCACCCGUGGUCA	1677	13482	UGACCACGGUGCAAAGCAG	3429
rs1803770	13465	UGCUUUGCACCCGUGGUCA	1678	13465	UGCUUUGCACCCGUGGUCA	1678	13483	CUGACCACGGUGCAAAGCA	3430
rs1803770	13466	GUUUGCACCCGUGGUCA	1679	13466	GUUUGCACCCGUGGUCA	1679	13484	UCUGACCACGGUGCAAAGC	3431
rs1803770	13467	CUUUGCACCCGUGGUCA	1680	13467	CUUUGCACCCGUGGUCA	1680	13485	CUCUGACCACGGUGCAAAG	3432
rs1803770	13468	UUUGCACCCGUGGUCA	1681	13468	UUUGCACCCGUGGUCA	1681	13486	CCUCUGACCACGGUGCAA	3433
rs1803770	13469	UUGCACCCGUGGUCA	1682	13469	UUGCACCCGUGGUCA	1682	13487	CCCUCUGACCACGGUGCAA	3434
rs1803770	13470	UGCACCCGUGGUCA	1683	13470	UGCACCCGUGGUCA	1683	13488	UCCUCUGACCACGGUGCA	3435
rs1803770	13471	GCACCCGUGGUCA	1684	13471	GCACCCGUGGUCA	1684	13489	GUCCUCUGACCACGGUGC	3436
rs1803770	13472	CACCCGUGGUCA	1685	13472	CACCCGUGGUCA	1685	13490	AGUCCUCUGACCACGGUG	3437
rs1803770	13473	ACCGUGGUCA	1686	13473	ACCGUGGUCA	1686	13491	CAGUCCUCUGACCACGGU	3438
rs1803770	13474	CCGUGGUCA	1687	13474	CCGUGGUCA	1687	13492	ACAGUCCUCUGACCACGG	3439
rs1803770	13475	CGUGGUCA	1688	13475	CGUGGUCA	1688	13493	GACAGUCCUCUGACCACG	3440
rs1803770	13476	GUGGUCA	1689	13476	GUGGUCA	1689	13494	UGACAGUCCUCUGACCAC	3441
rs1803770	13477	UGGUCA	1690	13477	UGGUCA	1690	13495	CUGACAGUCCUCUGACCA	3442
rs1803770	13478	GGUCAGAGGACUGUCAG	1691	13478	GGUCAGAGGACUGUCAG	1691	13496	GCUGACAGUCCUCUGACC	3443
rs1803770	13479	GUCAGAGGACUGUCAGU	1692	13479	GUCAGAGGACUGUCAGU	1692	13497	AGCUGACAGUCCUCUGAC	3444
rs1803770	13480	UCAGAGGACUGUCAGCUG	1693	13480	UCAGAGGACUGUCAGCUG	1693	13498	CAGCUGACAGUCCUCUGA	3445
rs1803770	13481	CAGAGGACUGUCAGCUGA	1694	13481	CAGAGGACUGUCAGCUGA	1694	13499	UCAGCUGACAGUCCUCUG	3446
rs1803770	13482	AGAGGACUGUCAGCUGAG	1695	13482	AGAGGACUGUCAGCUGAG	1695	13500	CUCAGCUGACAGUCCUCU	3447
rs1803770	13464	CUGCUUUGCACCCGUGGU	1696	13464	CUGCUUUGCACCCGUGGU	1696	13482	CGACCACGGUGCAAAGCAG	3448
rs1803770	13465	UGCUUUGCACCCGUGGU	1697	13465	UGCUUUGCACCCGUGGU	1697	13483	CCGACCACGGUGCAAAGCA	3449
rs1803770	13466	GUUUGCACCCGUGGU	1698	13466	GUUUGCACCCGUGGU	1698	13484	UCCGACCACGGUGCAAAGC	3450
rs1803770	13467	CUUUGCACCCGUGGU	1699	13467	CUUUGCACCCGUGGU	1699	13485	CUCCGACCACGGUGCAAAG	3451
rs1803770	13468	UUUGCACCCGUGGU	1700	13468	UUUGCACCCGUGGU	1700	13486	CCUCCGACCACGGUGCAA	3452
rs1803770	13469	UUGCACCCGUGGU	1701	13469	UUGCACCCGUGGU	1701	13487	CCCUCGACCACGGUGCAA	3453
rs1803770	13470	UGCACCCGUGGU	1702	13470	UGCACCCGUGGU	1702	13488	UCCUCCGACCACGGUGCA	3454
rs1803770	13471	GCACCCGUGGU	1703	13471	GCACCCGUGGU	1703	13489	GUCCUCCGACCACGGUGC	3455
rs1803770	13472	CACCCGUGGU	1704	13472	CACCCGUGGU	1704	13490	AGUCCUCCGACCACGGUG	3456
rs1803770	13473	ACCGUGGU	1705	13473	ACCGUGGU	1705	13491	CAGUCCUCCGACCACGGU	3457
rs1803770	13474	CCGUGGU	1706	13474	CCGUGGU	1706	13492	ACAGUCCUCCGACCACGG	3458
rs1803770	13475	CGUGGU	1707	13475	CGUGGU	1707	13493	GACAGUCCUCCGACCACG	3459
rs1803770	13476	GUGGU	1708	13476	GUGGU	1708	13494	UGACAGUCCUCCGACCAC	3460
rs1803770	13477	UGGU	1709	13477	UGGU	1709	13495	CUGACAGUCCUCCGACC	3461
rs1803770	13478	GGU	1710	13478	GGU	1710	13496	GCUGACAGUCCUCCGACC	3462
rs1803770	13479	GUCGAGGACUGUCAGU	1711	13479	GUCGAGGACUGUCAGU	1711	13497	AGCUGACAGUCCUCCGAC	3463
rs1803770	13480	UCGAGGACUGUCAGCUG	1712	13480	UCGAGGACUGUCAGCUG	1712	13498	CAGCUGACAGUCCUCCG	3464

rs1803770	13481	CGGAGGGACUGUCAGCUGA	1713	13481	CGGAGGGACUGUCAGCUGA	1713	13499	UCAGCUGACAGUCCCUCCG	3465
rs1803770	13482	GGAGGGACUGUCAGCUGAG	1714	13482	GGAGGGACUGUCAGCUGAG	1714	13500	CUCAGCUGACAGUCCCUCC	3466
rs1803771	13545	GGAGCCCCACCCAGACCUG	1715	13545	GGAGCCCCACCCAGACCUG	1715	13563	CAGGUCUGGGUGGGGCUCC	3467
rs1803771	13546	GAGCCCCACCCAGACCUGA	1716	13546	GAGCCCCACCCAGACCUGA	1716	13564	UCAGGUCUGGGUGGGGCU	3468
rs1803771	13547	AGCCCCACCCAGACCUGAA	1717	13547	AGCCCCACCCAGACCUGAA	1717	13565	UUCAGGUCUGGGUGGGGCU	3469
rs1803771	13548	GCCCCACCCAGACCUGAAU	1718	13548	GCCCCACCCAGACCUGAAU	1718	13566	AUUCAGGUCUGGGUGGGGC	3470
rs1803771	13549	CCCCACCCAGACCUGAAUG	1719	13549	CCCCACCCAGACCUGAAUG	1719	13567	CAUUCAGGUCUGGGUGGGG	3471
rs1803771	13550	CCCCACCCAGACCUGAAUGC	1720	13550	CCCCACCCAGACCUGAAUGC	1720	13568	GCAUUCAGGUCUGGGUGGG	3472
rs1803771	13551	CCACCCAGACCUGAAUGCU	1721	13551	CCACCCAGACCUGAAUGCU	1721	13569	AGCAUUCAGGUCUGGGUGG	3473
rs1803771	13552	CACCCAGACCUGAAUGCUU	1722	13552	CACCCAGACCUGAAUGCUU	1722	13570	AAGCAUUCAGGUCUGGGUG	3474
rs1803771	13553	ACCCAGACCUGAAUGCUUC	1723	13553	ACCCAGACCUGAAUGCUUC	1723	13571	GAAGCAUUCAGGUCUGGGU	3475
rs1803771	13554	CCAGACCUGAAUGCUUCU	1724	13554	CCAGACCUGAAUGCUUCU	1724	13572	AGAAGCAUUCAGGUCUGG	3476
rs1803771	13555	CCAGACCUGAAUGCUUCUG	1725	13555	CCAGACCUGAAUGCUUCUG	1725	13573	CAGAAGCAUUCAGGUCUG	3477
rs1803771	13556	CAGACCUGAAUGCUUCUGA	1726	13556	CAGACCUGAAUGCUUCUGA	1726	13574	UCAGAAGCAUUCAGGUCU	3478
rs1803771	13557	AGACCUGAAUGCUUCUGAG	1727	13557	AGACCUGAAUGCUUCUGAG	1727	13575	CUCAGAAGCAUUCAGGUC	3479
rs1803771	13558	GACCUGAAUGCUUCUGAGA	1728	13558	GACCUGAAUGCUUCUGAGA	1728	13576	UCUCAGAAGCAUUCAGGUC	3480
rs1803771	13559	ACCUGAAUGCUUCUGAGAG	1729	13559	ACCUGAAUGCUUCUGAGAG	1729	13577	CUCUCAGAAGCAUUCAGGU	3481
rs1803771	13560	CCUGAAUGCUUCUGAGAGC	1730	13560	CCUGAAUGCUUCUGAGAGC	1730	13578	GCUCUCAGAAGCAUUCAGG	3482
rs1803771	13561	CUGAAUGCUUCUGAGAGCA	1731	13561	CUGAAUGCUUCUGAGAGCA	1731	13579	UGCUCUCAGAAGCAUUCAG	3483
rs1803771	13562	UGAAUGCUUCUGAGAGCAA	1732	13562	UGAAUGCUUCUGAGAGCAA	1732	13580	UUGCUCUCAGAAGCAUUCA	3484
rs1803771	13563	GAUGCUUCUGAGAGCAAA	1733	13563	GAUGCUUCUGAGAGCAAA	1733	13581	UUUGCUCUCAGAAGCAUUC	3485
rs1803771	13545	GGAGCCCCACCCAGACCUGA	1734	13545	GGAGCCCCACCCAGACCUGA	1734	13563	UAGGUCUGGGUGGGGCUCC	3486
rs1803771	13546	GAGCCCCACCCAGACCUGAA	1735	13546	GAGCCCCACCCAGACCUGAA	1735	13564	UUAGGUCUGGGUGGGGCU	3487
rs1803771	13547	AGCCCCACCCAGACCUGAAA	1736	13547	AGCCCCACCCAGACCUGAAA	1736	13565	UUUAGGUCUGGGUGGGGCU	3488
rs1803771	13548	GCCCCACCCAGACCUGAAU	1737	13548	GCCCCACCCAGACCUGAAU	1737	13566	AUUUAGGUCUGGGUGGGGC	3489
rs1803771	13549	CCCCACCCAGACCUGAAUG	1738	13549	CCCCACCCAGACCUGAAUG	1738	13567	CAUUUAGGUCUGGGUGGGG	3490
rs1803771	13550	CCCACCCAGACCUGAAUGCU	1739	13550	CCCACCCAGACCUGAAUGCU	1739	13568	GCAUUUAGGUCUGGGUGGG	3491
rs1803771	13551	CCACCCAGACCUGAAUGCUU	1740	13551	CCACCCAGACCUGAAUGCUU	1740	13569	AGCAUUUAGGUCUGGGUGG	3492
rs1803771	13552	CACCCAGACCUGAAUGCUUC	1741	13552	CACCCAGACCUGAAUGCUUC	1741	13570	AAGCAUUUAGGUCUGGGUG	3493
rs1803771	13553	ACCCAGACCUGAAUGCUUCU	1742	13553	ACCCAGACCUGAAUGCUUCU	1742	13571	GAAGCAUUUAGGUCUGGGU	3494
rs1803771	13554	CCCAGACCUGAAUGCUUCU	1743	13554	CCCAGACCUGAAUGCUUCU	1743	13572	AGAAGCAUUUAGGUCUGGG	3495
rs1803771	13555	CCAGACCUGAAUGCUUCUG	1744	13555	CCAGACCUGAAUGCUUCUG	1744	13573	CAGAAGCAUUUAGGUCUGG	3496
rs1803771	13556	CAGACCUGAAUGCUUCUGA	1745	13556	CAGACCUGAAUGCUUCUGA	1745	13574	UCAGAAGCAUUUAGGUCUG	3497
rs1803771	13557	AGACCUGAAUGCUUCUGAG	1746	13557	AGACCUGAAUGCUUCUGAG	1746	13575	CUCAGAAGCAUUUAGGUCU	3498
rs1803771	13558	GACCUGAAUGCUUCUGAGA	1747	13558	GACCUGAAUGCUUCUGAGA	1747	13576	UCUCAGAAGCAUUUAGGUC	3499
rs1803771	13559	ACCUAAUGCUUCUGAGAG	1748	13559	ACCUAAUGCUUCUGAGAG	1748	13577	CUCUCAGAAGCAUUUAGGU	3500
rs1803771	13560	CCUAAUGCUUCUGAGAGC	1749	13560	CCUAAUGCUUCUGAGAGC	1749	13578	GCUCUCAGAAGCAUUUAGG	3501
rs1803771	13561	CUAAUGCUUCUGAGAGCA	1750	13561	CUAAUGCUUCUGAGAGCA	1750	13579	UGCUCUCAGAAGCAUUUAG	3502
rs1803771	13562	UAAUGCUUCUGAGAGCAA	1751	13562	UAAUGCUUCUGAGAGCAA	1751	13580	UUUGCUCUCAGAAGCAUUUA	3503

rs1803771	13563	AAAUGCUUCUGAGAGCAAA	1752	13563	AAAUGCUUCUGAGAGCAAA	1752	13581	UUUGCUCUCAGAGCAUUU	3504
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The 3'-ends of the Upper sequence and the Lower sequence of the siNA construct can include an overhang sequence, for example about 1, 2, 3, or 4 nucleotides in length, preferably 2 nucleotides in length, wherein the overhang sequence of the lower sequence is optionally complementary to a portion of the target sequence. The overhang can comprise the general structure B, BNN, NN, BNsN, or NsN, where B stands for any terminal cap moiety, N stands for any nucleotide (e.g., thymidine) and s stands for phosphorothioate or other internucleotide linkage as described herein (e.g. internucleotide linkage having Formula I). The upper sequence is also referred to as the sense strand, whereas the lower sequence is also referred to as the antisense strand. The upper and lower sequences in the Table can further comprise a chemical modification having Formulae I-VII or any combination thereof (see for example chemical modifications as shown in Table V herein).

Table III: HD synthetic siNA and Target Sequences

Target Pos	Target	SeqID	Sirna #	Aliases	Sequence	SeqID
586	CAAAGAAAGAACUUUCAGCUACC	3505	31993	HD:586U21 sense	AAGAAAGAACUUUCAGCUATT	3512
586	CAAAGAAAGAACUUUCAGCUACC	3505	31994	HD:604L21 (586C) antisense	UAGCUGAAAGUUUCUUUUUTT	3513
586	CAAAGAAAGAACUUUCAGCUACC	3505	31995	HD:586U21 stab04 sense	B AAGAAAGAACUUUCAGCUATT B	3514
586	CAAAGAAAGAACUUUCAGCUACC	3505	31996	HD:604L21 (586C) stab05 antisense	uAGcuGAAAGUUUUUUUUUtsT	3515
586	CAAAGAAAGAACUUUCAGCUACC	3505	31997	HD:586U21 stab07 sense	B AAGAAAGAACUUUCAGCUATT B	3516
586	CAAAGAAAGAACUUUCAGCUACC	3505	31998	HD:604L21 (586C) stab08 antisense	uAGcuGAAAGUUUUUUUUUtsT	3517
586	CAAAGAAAGAACUUUCAGCUACC	3505	31999	HD:586U21 inv sense	AUCGACUUUCAAAGAAAGAATT	3518
586	CAAAGAAAGAACUUUCAGCUACC	3505	32000	HD:604L21 (586C) inv antisense	UUUUUUUUUUGAAAGUUCGAUTT	3519
586	CAAAGAAAGAACUUUCAGCUACC	3505	32001	HD:586U21 inv stab04 sense	B AucGAcuuucAAAGAAAGAAATT B	3520
586	CAAAGAAAGAACUUUCAGCUACC	3505	32002	HD:604L21 (586C) inv stab05 antisense	uuuuuuuuGAAAAGucGauTsT	3521
586	CAAAGAAAGAACUUUCAGCUACC	3505	32003	HD:586U21 inv stab07 sense	B AucGAcuuucAAAGAAAGAAATT B	3522
586	CAAAGAAAGAACUUUCAGCUACC	3505	32004	HD:604L21 (586C) inv stab08 antisense	uuuuuuuuGAAAAGucGauTsT	3523
316	CCAUGGCGACCCUGGAAAAGCUG	3506	33065	HD:316U21 siRNA stab04 sense	B AuGGcGAcuuuGGAAAAAGcTT B	3524
591	AAAGAACUUUCAGCUACCAAGAA	3507	33066	HD:591U21 siRNA stab04 sense	B AGAAcuuuuAGcuAccAAAGTT B	3525
671	AAAUUCUCCAGAAUUUCAGAAAC	3508	33067	HD:671U21 siRNA stab04 sense	B AuucuccAGAAuuuucAGAAATT B	3526
769	AUUGCCUCAACAAAGUUUAUCAA	3509	33068	HD:769U21 siRNA stab04 sense	B uGccuccAAcAAAGuuuAucATT B	3527
1	GAGGAAGAGGAGGAGGCCGAC	3510	33069	HD-Ex58:3U21 siRNA stab04 sense	B GGAAGAGGAGGAGGccGAcTT B	3528
2	AAGAGGAGGAGGCCGACGCC	3511	33070	HD-Ex58:7U21 siRNA stab04 sense	B GAGGAGGAGGccGAcGccTT B	3529
316	CCAUGGCGACCCUGGAAAAGCUG	3506	33071	HD:334L21 siRNA (316C) stab05 antisense	GcuuuuccAGGGucGccAuTsT	3530
591	AAAGAACUUUCAGCUACCAAGAA	3507	33072	HD:609L21 siRNA (591C) stab05 antisense	cuuGGuAGcuGAAAguucuTsT	3531
671	AAAUUCUCCAGAAUUUCAGAAAC	3508	33073	HD:689L21 siRNA (671C) stab05 antisense	uuuGAAAUuuuGGAGAAuTsT	3532
769	AAUGCCUCAACAAAGUUUAUCAA	3509	33074	HD:787L21 siRNA (769C) stab05 antisense	uGAUAAcuuuGuuGAGGcATsT	3533
1	GAGGAAGAGGAGGAGGCCGAC	3510	33075	HD-Ex58:21L21 siRNA (Ex58-3C) stab05 antisense	GucGGccuccuccuuccTsT	3534
2	AAGAGGAGGAGGCCGACGCC	3511	33076	HD-Ex58:25L21 siRNA (Ex58-7C) stab05 antisense	GGGcGucGGccuccuccuuccTsT	3535
316	CCAUGGCGACCCUGGAAAAGCUG	3506	33077	HD:316U21 siRNA stab07 sense	B AuGGcGAcuuuGGAAAAAGcTT B	3536
591	AAAGAACUUUCAGCUACCAAGAA	3507	33078	HD:591U21 siRNA stab07 sense	B AGAAcuuuuAGcuAccAAAGTT B	3537
671	AAAUUCUCCAGAAUUUCAGAAAC	3508	33079	HD:671U21 siRNA stab07 sense	B AuucuccAGAAuuuucAGAAATT B	3538
769	AAUGCCUCAACAAAGUUUAUCAA	3509	33080	HD:769U21 siRNA stab07 sense	B uGccuccAAcAAAGuuuAucATT B	3539

1	GAGGAAGAGGAGGAGGCCGAC	3510	33081	HD-Ex58:3U21 siRNA stab07 sense	B GGAAGAGGAGGAGGCCGACTT B	3540
2	AAGAGGAGGAGGCCGACGCC	3511	33082	HD-Ex58:7U21 siRNA stab07 sense	B GAGGAGGAGGCCGACGCCTT B	3541
316	CCAUGGCGACCCUGGAAAGCUG	3506	33083	HD:334L21 siRNA (316C) stab08 antisense	GcuuuuccAGGGGucGccAuTsT	3542
591	AAAGAACUUUCAGGCUACCAAGAA	3507	33084	HD:609L21 siRNA (591C) stab08 antisense	cuuGGuAGcuGAAAGGuuucTsT	3543
671	AAUUUCUCCAGAAUUUCAGAAAC	3508	33085	HD:689L21 siRNA (671C) stab08 antisense	uuuGAAAUuucGGAGAAuTsT	3544
769	AAUGCCUCAACAAAGUUUAUCAA	3509	33086	HD:787L21 siRNA (769C) stab08 antisense	uGAUAAcuuuGuuGAGGcATsT	3545
1	GAGGAAGAGGAGGAGGCCGAC	3510	33087	HD-Ex58:21L21 siRNA (Ex58-3C) stab08 antisense	GucGGccuccuccuccuucTsT	3546
2	AAGAGGAGGAGGCCGACGCC	3511	33088	HD-Ex58:25L21 siRNA (Ex58-7C) stab08 antisense	GGGcGucGGccuccuccuucTsT	3547
316	CCAUGGCGACCCUGGAAAGCUG	3506	33089	HD:316U21 siRNA stab09 sense	B AUGGCGACCCUGGAAAGCCTT B	3548
591	AAAGAACUUUCAGCUACCAAGAA	3507	33090	HD:591U21 siRNA stab09 sense	B AGAACUUUCAGCUACCAAGTT B	3549
671	AAUUUCUCCAGAAUUUCAGAAAC	3508	33091	HD:671U21 siRNA stab09 sense	B AUUCUCCAGAAUUUCAGAAATT B	3550
769	AAUGCCUCAACAAAGUUUAUCAA	3509	33092	HD:769U21 siRNA stab09 sense	B UGCCUCAACAAAGUUUAUCATT B	3551
1	GAGGAAGAGGAGGAGGCCGAC	3510	33093	HD-Ex58:3U21 siRNA stab09 sense	B GGAAGAGGAGGAGGCCGACTT B	3552
2	AAGAGGAGGAGGCCGACGCC	3511	33094	HD-Ex58:7U21 siRNA stab09 sense	B GAGGAGGAGGCCGACGCCCTT B	3553
316	CCAUGGCGACCCUGGAAAGCUG	3506	33095	HD:334L21 siRNA (316C) stab10 antisense	GCUUUUCCAGGGGUCGCCAUTsT	3554
591	AAAGAACUUUCAGCUACCAAGAA	3507	33096	HD:609L21 siRNA (591C) stab10 antisense	CUUGGUAGCUGAAAGUUUCUTsT	3555
671	AAUUUCUCCAGAAUUUCAGAAAC	3508	33097	HD:689L21 siRNA (671C) stab10 antisense	UUCUGAAAUUCUGGAGAAUTsT	3556
769	AAUGCCUCAACAAAGUUUAUCAA	3509	33098	HD:787L21 siRNA (769C) stab10 antisense	UGAUAAcuuuGuuGAGGcATsT	3557
1	GAGGAAGAGGAGGAGGCCGAC	3510	33099	HD-Ex58:21L21 siRNA (Ex58-3C) stab10 antisense	GUCGGCCUCCUCCUUCUUCCTsT	3558
2	AAGAGGAGGAGGCCGACGCC	3511	33100	HD-Ex58:25L21 siRNA (Ex58-7C) stab10 antisense	GGGCGUCGGCCUCCUCCUUCCTsT	3559
Uppercase = ribonucleotide G = 2'-O-methyl Guanosine R = 5-bromo-deoxy-uridine						
u,c = 2'-deoxy-2'-fluoro U,C X = nitroindole universal base Z = sbl: symmetrical bifunctional linker						
T = thymidine Z = nitropyrrole universal base H = chol2: capped Cholesterol TEG						
B = inverted deoxy abasic Y = 3',3'-inverted thymidine A = 2'-O-methyl Adenosine						
s = phosphorothioate linkage M = glyceryl Q = L-uridine						
A = deoxy Adenosine N = 3'-O-methyl uridine						
G = deoxy Guanosine P = L-thymidine						

Table IV

Non-limiting examples of Stabilization Chemistries for chemically modified siNA constructs

Chemistry	pyrimidine	Purine	cap	p=S	Strand
“Stab 00”	Ribo	Ribo	TT at 3'-ends		S/AS
“Stab 1”	Ribo	Ribo	-	5 at 5'-end 1 at 3'-end	S/AS
“Stab 2”	Ribo	Ribo	-	All linkages	Usually AS
“Stab 3”	2'-fluoro	Ribo	-	4 at 5'-end 4 at 3'-end	Usually S
“Stab 4”	2'-fluoro	Ribo	5' and 3'-ends	-	Usually S
“Stab 5”	2'-fluoro	Ribo	-	1 at 3'-end	Usually AS
“Stab 6”	2'-O-Methyl	Ribo	5' and 3'-ends	-	Usually S
“Stab 7”	2'-fluoro	2'-deoxy	5' and 3'-ends	-	Usually S
“Stab 8”	2'-fluoro	2'-O-Methyl	-	1 at 3'-end	Usually AS
“Stab 9”	Ribo	Ribo	5' and 3'-ends	-	Usually S
“Stab 10”	Ribo	Ribo	-	1 at 3'-end	Usually AS
“Stab 11”	2'-fluoro	2'-deoxy	-	1 at 3'-end	Usually AS
“Stab 12”	2'-fluoro	LNA	5' and 3'-ends		Usually S
“Stab 13”	2'-fluoro	LNA		1 at 3'-end	Usually AS
“Stab 14”	2'-fluoro	2'-deoxy		2 at 5'-end 1 at 3'-end	Usually AS
“Stab 15”	2'-deoxy	2'-deoxy		2 at 5'-end 1 at 3'-end	Usually AS
“Stab 16”	Ribo	2'-O-Methyl	5' and 3'-ends		Usually S
“Stab 17”	2'-O-Methyl	2'-O-Methyl	5' and 3'-ends		Usually S
“Stab 18”	2'-fluoro	2'-O-Methyl	5' and 3'-ends	1 at 3'-end	Usually S
“Stab 19”	2'-fluoro	2'-O-Methyl	3'-end		Usually AS
“Stab 20”	2'-fluoro	2'-deoxy	3'-end		Usually AS
“Stab 21”	2'-fluoro	Ribo	3'-end		Usually AS
“Stab 22”	Ribo	Ribo	3'-end -		Usually AS

CAP = any terminal cap, see for example **Figure 10**.

All Stab 1-22 chemistries can comprise 3'-terminal thymidine (TT) residues

All Stab 1-22 chemistries typically comprise about 21 nucleotides, but can vary as described herein.

S = sense strand

AS = antisense strand

Table V**A. 2.5 μ mol Synthesis Cycle ABI 394 Instrument**

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	6.5	163 μ L	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	23.8	238 μ L	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 μ L	5 sec	5 sec	5 sec
N-Methyl Imidazole	186	233 μ L	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
Iodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 μ L	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	NA	NA	NA

B. 0.2 μ mol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'-O-methyl	Wait Time*RNA
Phosphoramidites	15	31 μ L	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 μ L	45 sec	233 min	465 sec
Acetic Anhydride	655	124 μ L	5 sec	5 sec	5 sec
N-Methyl Imidazole	1245	124 μ L	5 sec	5 sec	5 sec
TCA	700	732 μ L	10 sec	10 sec	10 sec
Iodine	20.6	244 μ L	15 sec	15 sec	15 sec
Beaucage	7.7	232 μ L	100 sec	300 sec	300 sec
Acetonitrile	NA	2.64 mL	NA	NA	NA

C. 0.2 μ mol Synthesis Cycle 96 well Instrument

Reagent	Equivalents:DNA/ 2'-O-methyl/Ribo	Amount: DNA/2'-O- methyl/Ribo	Wait Time* DNA	Wait Time* 2'-O- methyl	Wait Time* Ribo
Phosphoramidites	22/33/66	40/60/120 μ L	60 sec	180 sec	360sec
S-Ethyl Tetrazole	70/105/210	40/60/120 μ L	60 sec	180 min	360 sec
Acetic Anhydride	265/265/265	50/50/50 μ L	10 sec	10 sec	10 sec
N-Methyl Imidazole	502/502/502	50/50/50 μ L	10 sec	10 sec	10 sec
TCA	238/475/475	250/500/500 μ L	15 sec	15 sec	15 sec
Iodine	6.8/6.8/6.8	80/80/80 μ L	30 sec	30 sec	30 sec
Beaucage	34/51/51	80/120/120	100 sec	200 sec	200 sec
Acetonitrile	NA	1150/1150/1150 μ L	NA	NA	NA

- 5
- Wait time does not include contact time during delivery.
 - Tandem synthesis utilizes double coupling of linker molecule